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* * * * * * * * * *  Welcome to STN International  * * * * * * * * * *

NEWS  1          Web Page URLs for STN Seminar Schedule - N. America
NEWS  2          "Ask CAS" for self-help around the clock
NEWS  3  JAN 27  Source of Registration (SR) information in REGISTRY updated
                 and searchable
NEWS  4  JAN 27  A new search aid, the Company Name Thesaurus, available in
                 CA/CAplus
NEWS  5  FEB 05  German (DE) application and patent publication number format
                 changes
NEWS  6  MAR 03  MEDLINE and LMEDLINE reloaded
NEWS  7  MAR 03  MEDLINE file segment of TOXCENTER reloaded
NEWS  8  MAR 03  FRANCEPAT now available on STN
NEWS  9  MAR 29  Pharmaceutical Substances (PS) now available on STN
NEWS 10  MAR 29  WPIFV now available on STN
NEWS 11  MAR 29  New monthly current-awareness alert (SDI) frequency in RAPRA
NEWS 12  APR 26  PROMT: New display field available
NEWS 13  APR 26  IFIPAT/IFIUDB/IFICDB: New super search and display field
                 available
NEWS 14  APR 26  LITALERT now available on STN
NEWS 15  APR 27  NLDB: New search and display fields available
NEWS 16  May 10  PROUSDDR now available on STN
NEWS 17  May 19  PROUSDDR: One FREE connect hour, per account, in both May
                 and June 2004
NEWS 18  May 12  EXTEND option available in structure searching
NEWS 19  May 12  Polymer links for the POLYLINK command completed in REGISTRY
NEWS 20  May 17  FRFULL now available on STN
NEWS 21  May 27  STN User Update to be held June 7 and June 8 at the SLA 2004
                 Conference
NEWS 22  May 27  New UPM (Update Code Maximum) field for more efficient patent
                 SDIs in CAplus
NEWS 23  May 27  CAplus super roles and document types searchable in REGISTRY
NEWS 24  May 27  Explore APOLLIT with free connect time in June 2004

NEWS EXPRESS  MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT
              MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
              AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004
NEWS HOURS    STN Operating Hours Plus Help Desk Availability
NEWS INTER    General Internet Information
NEWS LOGIN    Welcome Banner and News Items
NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
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FILE 'HOME' ENTERED AT 20:39:06 ON 08 JUN 2004

=> index biosci

FILE 'DRUGMONOG' ACCESS NOT AUTHORIZED
COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
                                                       ENTRY    SESSION
FULL ESTIMATED COST                                     0.21       0.21

INDEX 'ADISCTI, ADISINSIGHT, ADISNEWS, AGRICOLA, ANABSTR, AQUASCI, BIOBUSINESS,
      BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO, CABA, CANCERLIT,
      CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS, DDFB, DDFU,
      DGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 20:39:16 ON 08 JUN 2004

70 FILES IN THE FILE LIST IN STNINDEX

Enter SET DETAIL ON to see search term postings or to view
search error messages that display as 0* with SET DETAIL OFF.

=> s (thermogenic (w) protein) (p) (skunk (w) cabbage)
          0*  FILE ADISNEWS
          0*  FILE BIOCOMMERCE
          0*  FILE BIOTECHABS
          0*  FILE BIOTECHDS
          0*  FILE BIOTECHNO
          0*  FILE CEABA-VTB
          0*  FILE CIN
  25 FILES SEARCHED...
          0*  FILE ESBIOBASE
          0*  FILE FEDRIP
          0*  FILE FOMAD
          0*  FILE FOREGE
          0*  FILE FROSTI
          0*  FILE FSTA
          1   FILE IFIPAT
          0*  FILE KOSMET
          0*  FILE MEDICONF
          0*  FILE NTIS
          0*  FILE NUTRACEUT
          0*  FILE PASCAL
          0*  FILE PHARMAML
  62 FILES SEARCHED...

   1 FILES HAVE ONE OR MORE ANSWERS,   70 FILES SEARCHED IN STNINDEX

L1   QUE (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

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COST IN U.S. DOLLARS                                SINCE FILE      TOTAL
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FULL ESTIMATED COST                                     1.14       1.35

FILE 'IFIPAT' ENTERED AT 20:40:37 ON 08 JUN 2004
COPYRIGHT (C) 2004 IFI CLAIMS(R) Patent Services (IFI)

FILE COVERS 1950 TO PATENT PUBLICATION DATE: 3 Jun 2004 (20040603/PD)
FILE LAST UPDATED: 4 Jun 2004 (20040604/ED)
HIGHEST GRANTED PATENT NUMBER: US2004087609
HIGHEST APPLICATION PUBLICATION NUMBER: US2004107471
UNITERM INDEXING IS AVAILABLE IN THE IFIUDB FILE
UNITERM INDEXING LAST UPDATED: 27 May 2004 (20040527/UP)
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INDEXING CURRENT THROUGH PAT PUB DATE: 25 Nov 2003 (20031125/PD)

IFIPAT has been reloaded (12/21/2003). See HELP RLOAD for details.

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=> s l1
           64 THERMOGENIC
        65668 PROTEIN
           37 SKUNK
          450 CABBAGE
L2          1 (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)

=> d l2 bib ab

L2   ANSWER 1 OF 1  IFIPAT  COPYRIGHT 2004 IFI on STN
AN    10560887  IFIPAT;IFIUDB;IFICDB
TI    PLANT THERMOGENIC GENES AND PROTEINS
INF   Ito; Kikukatsu, Iwate, JP
IN    Ito Kikukatsu (JP)
PAF   Unassigned
PA    Unassigned Or Assigned To Individual (68000)
AG    WENDEROTH, LIND & PONACK, L.L.P., 2033 K STREET N. W., SUITE 800,
      WASHINGTON, DC, 20006-1021, US
PI    US 2004068105   A1  20040408
AI    US 2003-671628      20030929
RLI   WO 2000-JP3806      20000612 Section 371 PCT Filing UNKNOWN
      US 2002-9962        20020123 DIVISION
PRAI  JP 1999-167439      19990614
FI    US 2004068105       20040408
DT    Utility; Patent Application - First Publication
FS    CHEMICAL
      APPLICATION
CLMN  6
GI     8 Figure(s).
```

FIG. 1 shows the change of the temperature of the spadix in skunk cabbage and that of ambient temperature with a lapse of time.

FIG. 2 shows the results of northern blotting, indicating the expression profile of SfUCPa (A) and SfUCPb (B) in the spadix and leaf of skunk cabbage at room temperature (RI) and during cold treatment (4 degrees C. for 3 days). The lower figures respectively show the results of ethidium bromide staining of non-decomposed rRNA.

FIG. 3 compares the alignment of amino acid sequences of SfUCPA and SfUCPB, together with potato UCP (StUCP), Arabidopsis UCP (AtPUMP) and human UCP. The asterisk (*) attached under the sequences indicate the same amino acid sequence, and the dot (.) indicates the conservative change in all of the sequences. The boldface indicates the same sequence between SfUCPA and SfUCPB. The gap introduced to optimize the sequence alignment is indicated by a dash (-). The alignment was made using a CLUSTAL W program. The characteristic domains of energy transfer proteins typical of mitochondria are surrounded by a square. The shaded bars (I-VI) above the upper sequence show estimated transmembrane domains.

FIG. 4 shows a hydrophobic plot of SfUCPA. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are indicated by TM1 to TM6.

FIG. 5 shows a diagrammatic illustration of SfUCPA topology in the mitochondria membrane.

FIG. 6 shows a hydrophobic plot of SfUCPB. The vertical axis indicates the degree of hydrophobicity and the estimated transmembrane domains are indicated by TM1 to TM4 and TM6.

FIG. 7 shows a diagrammatic illustration of SfUCPB topology in the mitochondria membrane.

FIG. 8 shows the results of in vitro translation using respective cDNAs of the genes SfUCPa and SfUCPb as templates. () indicates a control, S a sense RNA, and AS an antisense RNA. The asterisk (*) indicates a non-specific product and the empty circle denotes the position of a low molecular translated artificial product synthesized from a small ORF.

AB Th inventions of his application include thermogenic genes named SfUCPa and SfUCPb which are derived from skunk cabbage. cDNA of each gene comprises the base sequence of SEQ ID NO: 1 and 3, respectively. Thermogenic proteins, SfUCPA and SfUCPB, are expressed from genes SfUCPa and SfUCPb, comprises the amino acid sequence of SEQ ID NO: 2 and 4.

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=> d his

     (FILE 'HOME' ENTERED AT 20:39:06 ON 08 JUN 2004)

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     CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB, CROPU, DISSABS,
     DDFB, DDFU, DGENE, DRUGB, DRUGMONOG2, ...' ENTERED AT 20:39:16 ON 08 JUN
     2004
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              0*  FILE PASCAL
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L1             QUE (THERMOGENIC (W) PROTEIN) (P) (SKUNK (W) CABBAGE)
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L2            1 S L1

=> log y
COST IN U.S. DOLLARS                                  SINCE FILE      TOTAL
                                                         ENTRY    SESSION
FULL ESTIMATED COST                                       5.91       7.26
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STN INTERNATIONAL LOGOFF AT 20:40:57 ON 08 JUN 2004

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 16:59:57 ; Search time 5858.22 Seconds
(without alignments)
11282.980 Million cell updates/sec

Title: US-10-671-628-1
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
3: gb_in:*
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14: gb_vi:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
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29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1525	100.0	1525	6	E50743	E50743 Plant exoth
2	1525	100.0	1525	6	BD011855	BD011855 Thermogen
3	1525	100.0	1525	8	AB024733	AB024733 Symplocar
4	1076.6	70.6	2991	6	E50744	E50744 Plant exoth
5	1076.6	70.6	2991	6	BD011856	BD011856 Thermogen
6	1076.6	70.6	2991	8	AB024734	AB024734 Symplocar
7	646.4	42.4	1209	8	AB088762	AB088762 Helicodic
8	537	35.2	1429	8	AF472619	AF472619 Lycopersi
9	537	35.2	1434	8	STUCPMRNA	Y11220 Solanum tub
10	502.4	32.9	1240	8	ATMTUNCOU	AJ001264 Arabidops
11	500.8	32.8	920	6	AX651736	AX651736 Sequence
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16	500.8	32.8	1225	8	ATPUMP	AJ223983 Arabidops
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19	473	31.0	1088	6	AX269362	AX269362 Sequence
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21	471.4	30.9	1227	8	AY088200	AY088200 Arabidops
22	443.2	29.1	1263	8	AK061318	AK061318 Oryza sat
23	441.6	29.0	1179	8	AK104090	AK104090 Oryza sat
24	437.2	28.7	1243	8	AF461732	AF461732 Zea mays
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26	415.4	27.2	974	6	AX269364	AX269364 Sequence
27	415.4	27.2	974	8	AB042428	AB042428 Triticum
28	410.6	26.9	971	8	AB042429	AB042429 Triticum
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32	188.6	12.4	1992	5	BC044682	BC044682 Xenopus l
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34	176.8	11.6	1565	5	CCA243486	AJ243486 Cyprinus
35	176.6	11.6	1483	5	BC056737	BC056737 Danio rer
36	174	11.4	1698	5	BC053173	BC053173 Danio rer

37	173.4	11.4	1439	5	DRE243250	AJ243250 Danio rer
38	169.4	11.1	2009	5	BC063352	BC063352 Silurana
39	163	10.7	1949	6	AR064042	AR064042 Sequence
40	163	10.7	1949	6	AR074015	AR074015 Sequence
41	163	10.7	1949	6	BD075717	BD075717 UCP3 gene
42	162.2	10.6	1357	10	AF032902	AF032902 Mus muscu
43	161	10.6	943	10	AY326457	AY326457 Dicroston
44	160.6	10.5	927	10	AB008216	AB008216 Mus muscu
45	160.6	10.5	979	10	AF030164	AF030164 Mus muscu

ALIGNMENTS

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RESULT 1
E50743
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DEFINITION  Plant exotherm-related gene and exotherm-related protein.
ACCESSION   E50743
VERSION     E50743.1  GI:18622139
KEYWORDS    JP 2000354489-A/1.
SOURCE      Symplocarpus foetidus
  ORGANISM  Symplocarpus foetidus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
REFERENCE   1  (bases 1 to 1525)
  AUTHORS   Ito,K.
  TITLE     Plant exotherm-related gene and exotherm-related protein
  JOURNAL   Patent: JP 2000354489-A 1 26-DEC-2000;
            SCIENCE & TECH AGENCY
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            PN   JP 2000354489-A/1
            PD   26-DEC-2000
            PF   14-JUN-1999 JP 1999167439
            PR
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ORIGIN

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Qy         61 AATTGCAGTTTTTCGCAGCGGCGTCATCATCAAGACCCTCCGCCTTTCCGCGCCAAACGC 120
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        841 GCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGACAATCTTAAAA 900
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        961 TTTGCCGTCTGTATCGGTTCTCCTGTTGATGTGATGAAGTCTAGAATGATGGGAGATTCA 1020
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Qy       1021 GCCTACAAAAGCACATTTGATTGTTTCATCAAGACATTGAAAAATGATGGGCTTCTTGCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1261 GCGAGAGACAAATAAATCTTCCTGACTGCTCAGATGTGTACCTTTTTTATGAATGGTTCT 1320
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTCTGCTGCTAATCTTGGTAGGAGAAGAAAAGTCTTACATTGAGTGATAACGTTGTTCT 1440

Qy       1441 CTGCATCCATTATTTTTCAGAGATACTATTTGACACATGAAAAGTAATGCACATCAGGTT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTGCATCCATTATTTTTCAGAGATACTATTTGACACATGAAAAGTAATGCACATCAGGTT 1500

Qy       1501 TTTTTTAAAAAAAAAAAAAAAAAAA 1525
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Db       1501 TTTTTTAAAAAAAAAAAAAAAAAAA 1525
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RESULT 2
BD011855

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LOCUS       BD011855                1525 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  Thermogenesis genes and thermogenesis proteins in plant.
ACCESSION   BD011855
VERSION     BD011855.1  GI:22092044
KEYWORDS    WO 0077211-A/1.
SOURCE      Symplocarpus foetidus
  ORGANISM  Symplocarpus foetidus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
REFERENCE   1  (bases 1 to 1525)
  AUTHORS   Ito,K.
  TITLE     Thermogenesis genes and thermogenesis proteins in plant
  JOURNAL   Patent: WO 0077211-A 1 21-DEC-2000;
            JAPAN SCIENCE AND TECHNOLOGY CORP,KIKUKATSU ITO
COMMENT     OS   Symplocarpus foetidus
            PN   WO 0077211-A/1
            PD   21-DEC-2000
            PF   12-JUN-2000 WO 2000JP003806
            PR   14-JUN-1999 JP 99P   167439
            PI   KIKUKATSU ITO
            PC   C12N15/29,C07K14/415
            CC
            FH   Key             Location/Qualifiers
            FT   CDS             (280). .(1188)
            FT   polyA_site      (1271). .(1276).
FEATURES             Location/Qualifiers
     source          1. .1525
                     /organism="Symplocarpus foetidus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:28477"
ORIGIN
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Query Match 100.0%; Score 1525; DB 6; Length 1525;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGGATTCGCAGAAGAAAGGCCAGAACCCGATTCCTTCCCGTCTTCTTCTCCTTCCGCCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGATTCGCAGAAGAAAGGCCAGAACCCGATTCCTTCCCGTCTTCTTCTCCTTCCGCCC 60

Qy         61 AATTGCAGTTTTTCGCAGCGGCGTCATCATCAAGACCCTCCGCCTTTCCGCGCCAAACGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTGCAGTTTTTCGCAGCGGCGTCATCATCAAGACCCTCCGCCTTTCCGCGCCAAACGC 120

Qy        121 CTTCCACCCCCACCCAATCGCCCTCCGTTTCCCGAAATATTCCTCTTCCCTCCTCCCTTT 180
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Db        121 CTTCCACCCCCACCCAATCGCCCTCCGTTTCCCGAAATATTCCTCTTCCCTCCTCCCTTT 180

Qy        181 TCTTCTCTACATAAACCCTAACCACCCCATCCTCTCCTCCCGCTTCCGACCACCCTGCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCTTCTCTACATAAACCCTAACCACCCCATCCTCTCCTCCCGCTTCCGACCACCCTGCAT 240

Qy        241 TCTACTGGGAGCCCATTTGATCGAGGTTTCCCGGCGAGGATGGGCGATCACGGCCCGAGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTACTGGGAGCCCATTTGATCGAGGTTTCCCGGCGAGGATGGGCGATCACGGCCCGAGG 300

Qy        301 ACCGAGATCTCGTTTGCCGGCAGTTCGCGAGCAGCATTCGCCGCTTGCTTCGCCGAGCTT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCGAGATCTCGTTTGCCGGCAGTTCGCGAGCAGCATTCGCCGCTTGCTTCGCCGAGCTT 360

Qy        361 TGCACGATTCCGTTGGACACTGCTAAAGTTAGGCTTCAACTCCAAAAGAAAGCAGTAACA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCACGATTCCGTTGGACACTGCTAAAGTTAGGCTTCAACTCCAAAAGAAAGCAGTAACA 420

Qy        421 GGTGATGTGGTGGCTTTGCCAAAATACAGGGGAATGTTGGGCACTGTTGCCACTATTGCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGATGTGGTGGCTTTGCCAAAATACAGGGGAATGTTGGGCACTGTTGCCACTATTGCC 480

Qy        481 AGGGAGGAAGGTTTGTCGGCACTCTGGAAAGGAATTGTACCCGGTTTGCATCGTCAATGC 540
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Db        481 AGGGAGGAAGGTTTGTCGGCACTCTGGAAAGGAATTGTACCCGGTTTGCATCGTCAATGC 540

Qy        541 CTCTTTGGAGGGCTACGAATTGGGTTGTATGAACCAGTTAAGTCCTTTTATGTTGGAGAT 600
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Db        541 CTCTTTGGAGGGCTACGAATTGGGTTGTATGAACCAGTTAAGTCCTTTTATGTTGGAGAT 600

Qy        601 AACTTTGTTGGAGATATTCCTTTATCCAAGAAAATACTTGCTGGGCTTACAACAGGTGCA 660
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Db        601 AACTTTGTTGGAGATATTCCTTTATCCAAGAAAATACTTGCTGGGCTTACAACAGGTGCA 660

Qy        661 TTAGCAATTATAGTGGCAAATCCCACTGACCTTGTTAAAGTTCGACTTCAATCTGAAGGT 720
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Db        661 TTAGCAATTATAGTGGCAAATCCCACTGACCTTGTTAAAGTTCGACTTCAATCTGAAGGT 720

Qy        721 AAACTCCCCCCTGGGGTACCGAGACGTTATTCAGGGGCGCTAAATGCTTATTCAACCATA 780
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Db        721 AAACTCCCCCCTGGGGTACCGAGACGTTATTCAGGGGCGCTAAATGCTTATTCAACCATA 780

Qy        781 GTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCCCGCAAT 840
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Db        781 GTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCCCGCAAT 840

Qy        841 GCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGACAATCTTAAAA 900
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Db        841 GCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGACAATCTTAAAA 900

Qy        901 TTACCAGGATTCTCAGATAATATTTTTACTCATATTTTAGCCGGTCTGGGGGCAGGTTTT 960
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Db        901 TTACCAGGATTCTCAGATAATATTTTTACTCATATTTTAGCCGGTCTGGGGGCAGGTTTT 960

Qy        961 TTTGCCGTCTGTATCGGTTCTCCTGTTGATGTGATGAAGTCTAGAATGATGGGAGATTCA 1020
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Db        961 TTTGCCGTCTGTATCGGTTCTCCTGTTGATGTGATGAAGTCTAGAATGATGGGAGATTCA 1020

Qy       1021 GCCTACAAAAGCACATTTGATTGTTTCATCAAGACATTGAAAAATGATGGGCTTCTTGCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCTACAAAAGCACATTTGATTGTTTCATCAAGACATTGAAAAATGATGGGCTTCTTGCT 1080

Qy       1081 TTTTACAAGGGGTTTATCCCAAACTTTGGTCGGTTAGGATCGTGGAATGTGATCATGTTT 1140
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Db       1081 TTTTACAAGGGGTTTATCCCAAACTTTGGTCGGTTAGGATCGTGGAATGTGATCATGTTT 1140

Qy       1141 TTGACCTTGGAGCAGGTCAAGAAGTTTTTCATCAAAGAGGTGCCAAATTAATACATTGAA 1200
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Db       1141 TTGACCTTGGAGCAGGTCAAGAAGTTTTTCATCAAAGAGGTGCCAAATTAATACATTGAA 1200

Qy       1201 CTCGGATAGGAGTAGAAAGAAAGGGTTTTTGTGGAATTTTCTCTACCGGTGTGGATCCTG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CTCGGATAGGAGTAGAAAGAAAGGGTTTTTGTGGAATTTTCTCTACCGGTGTGGATCCTG 1260

Qy       1261 GCGAGAGACAAATAAATCTTCCTGACTGCTCAGATGTGTACCTTTTTTATGAATGGTTCT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GCGAGAGACAAATAAATCTTCCTGACTGCTCAGATGTGTACCTTTTTTATGAATGGTTCT 1320

Qy       1321 TTTCTTATAGAGGACAGAGAAAAGAAAAAAAAAAATCATTGTCATTTACTCTTTTTCCCCA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTCTTATAGAGGACAGAGAAAAGAAAAAAAAAAATCATTGTCATTTACTCTTTTTCCCCA 1380
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Qy       1381 TTTCTGCTGCTAATCTTGGTAGGAGAAGAAAAGTCTTACATTGAGTGATAACGTTGTTCT 1440
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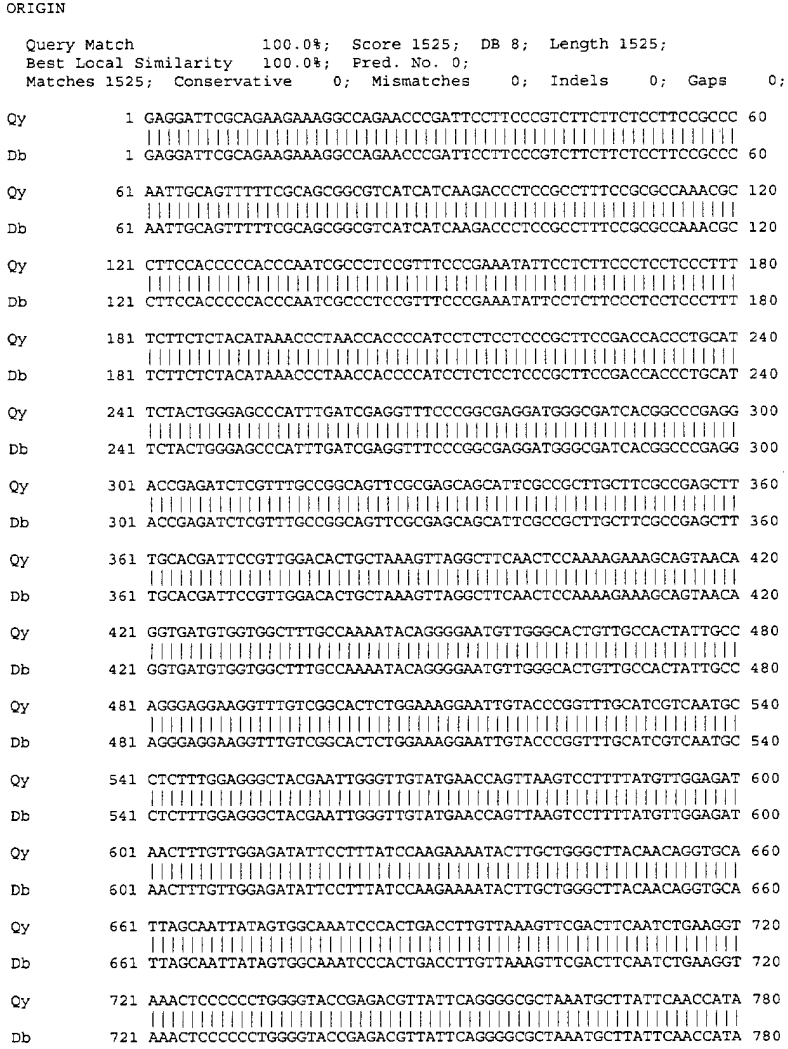
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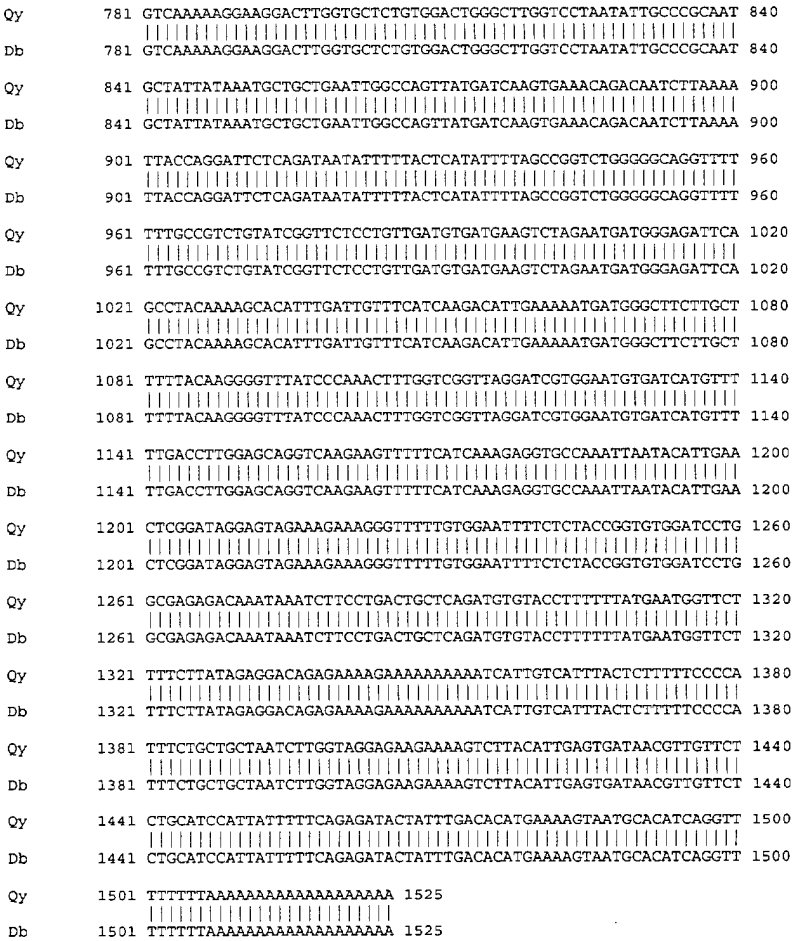
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Db       1501 TTTTTTAAAAAAAAAAAAAAAAAAA 1525
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RESULT 3
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LOCUS       AB024733               1525 bp    mRNA    linear   PLN 26-JUL-2002
DEFINITION  Symplocarpus foetidus mRNA for SfUCPa, complete cds.
ACCESSION   AB024733
VERSION     AB024733.1  GI:7106156
KEYWORDS    .
SOURCE      Symplocarpus foetidus
  ORGANISM  Symplocarpus foetidus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
REFERENCE   1
  AUTHORS   Ito,K.
  TITLE     Isolation of two distinct cold-inducible cDNAs encoding plant
            uncoupling proteins from the spadix of skunk cabbage (Symplocarpus
            foetidus)
  JOURNAL   Plant Sci. 149, 167-173 (1999)
REFERENCE   2  (bases 1 to 1525)
  AUTHORS   Ito,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAR-1999) Kikukatsu Ito, Cryobiosystem Research
            Center, Iwate Univ., Division of Biosystem and Bioresource
            Technology; 3-18-8, Ueda, Morioka 020-8550, Japan
            (E-mail:kikuito@iwate-u.ac.jp, Tel:81-19-621-6253)
FEATURES             Location/Qualifiers
     source          1. .1525
                     /organism="Symplocarpus foetidus"
                     /mol_type="mRNA"
                     /db_xref="taxon:28477"
     gene            1. .1525
                     /gene="SfUCPa"
     CDS             280. .1191
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                     LNAYSTIVKKEGLGALWTGLGPNIARNAIINAAELASYDQVKQTILKLPGFSDNIFTH
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ORIGIN

Query Match 100.0%; Score 1525; DB 8; Length 1525;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;





RESULT 4
E50744
LOCUS E50744 2991 bp DNA linear PAT 31-JAN-2002

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DEFINITION  Plant exotherm-related gene and exotherm-related protein.
ACCESSION   E50744
VERSION     E50744.1  GI:18622140
KEYWORDS    JP 2000354489-A/2.
SOURCE      Symplocarpus foetidus
  ORGANISM  Symplocarpus foetidus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
REFERENCE   1  (bases 1 to 2991)
  AUTHORS   Ito,K.
  TITLE     Plant exotherm-related gene and exotherm-related protein
  JOURNAL   Patent: JP 2000354489-A 2 26-DEC-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS   Symplocarpus foetidus
            PN   JP 2000354489-A/2
            PD   26-DEC-2000
            PF   14-JUN-1999 JP 1999167439
            PR
            PI   KIKUICHI ITO
            PC   C12N15/09,C07K14/415//A01H5/00,A61K31/00,A61K31/00,A61K38/00,
            PC   C12P21/02,
            PC   C12N15/00,A61K37/02
            CC
            FH   Key             Location/Qualifiers
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            FT   polyA_site      (1171). .(1176)
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FEATURES             Location/Qualifiers
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Query Match 70.6%; Score 1076.6; DB 6; Length 2991;
Best Local Similarity 86.6%; Pred. No. 4.4e-263;
Matches 1357; Conservative 0; Mismatches 49; Indels 161; Gaps 9;

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Qy          1 GAGGATTCGCAGAAGAAAGGCCAGAACCCGATTCCTTCCCGTCTTCTTCTCCTTCCGCCC 60
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Db         18 GAGGATTCGCAGAAGAAAGGCCAGAACCCGATTCCTTCCCGTCTTCTTCTCCTTCCGCCC 77

Qy         61 AATTGCAGTTTTTCGCAGCGGCGTCATCATCAAGACCCTCCGCCTTTCCGCGCCAAACGC 120
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Db         78 AATTGCAGTTTTTCGCAGCGG-GTCATCATCAAGACCCTCCGCCTTTCCGCGCCAAACGC 136

Qy        121 CTTCCACCCCCACCCAATCGCCCTCCGTTTCCCGAAATATTCCTCTTCCCTCCTCCCTTT 180
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Db        137 CTTCCACCC--------AATCCCTCCGTTTCCCGAAATATTCCCCTTC---CCTCCCTTT 185

Qy        181 TCTTCTCTACATAAACCCTAACCA-CCCCATCCTCTCCTCCCGCTTCCGACCACCCTGCA 239
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        186 TCTTCTCTACATAAACCCTAACCACCCCCATCCTCTCCTCCCGCTTCCGACCACCCTGCA 245

Qy        240 TTCTACTGGGAGCCCATTTGATCGAGGTTTCCCGGCGAGGATGGGCGATCACGGCCCGAG 299
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Db        246 TTCTACTGGGATCCCATTTGATCGACGTTTCCCGGCGAGGATGGGCGATCACGGCCCGAG 305

Qy        300 GACCGAGATCTCGTTTGCCGGCAGTTCGCGAGCAGCATTCGCCGCTTGCTTCGCCGAGCT 359
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Db        306 GACCGAGATCTCGTTTGCCGGCAGTTCGCGAGCAGCATTCGCCGCTTGCTTCGCCGAGCT 365

Qy        360 TTGCACGATTCCGTTGGACACTGCTAAAGTTAGGCTTCAACTCCAAAAGAAAGCAGTAAC 419
              || |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        366 CTGTACGATTCCGTTGGACACTGCTAAAGTTAGGCTTCAGCTCCAAAAGAAAGCAGTAAC 425

Qy        420 AGGTGATGTGGTGGCTTTGCCAAAATACAGGGGAATGTTGGGCACTGTTGCCACTATTGC 479
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Db        426 AGGTGATGTGGTGGCTTTGCCAAAATACAGGGGAATGTTGGGCACTGTTGCCACTATTGC 485

Qy        480 CAGGGAGGAAGGTTTGTCGGCACTCTGGAAAGGAATTGTACCCGGTTTGCATCGTCAATG 539
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Db        486 CAGGGAGGAAGGTTTGTCGGCACTCTGGAAAGGAATTGTACCCGGTTTGCATCGTCAATG 545

Qy        540 CCTCTTTGGAGGGCTACGAATTGGGTTGTATGAACCAGTTAAGTCCTTTTATGTTGGAGA 599
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Db        546 CCTCTTTGGAGGGCTACGAATTGGGTTGTATGAACCAGTTAAGTCCTTTTATGTTGGAGA 605

Qy        600 TAACTTTGTTGGAGATATTCCTTTATCCAAGAAAATACTTGCTGGGCTTACAACAGGTGC 659
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Db        606 TAACTTTGTTGGAGATATTCCTTTATCCAAGAAAATACTTGCTGGGCTTACAACAGGTGC 665

Qy        660 ATTAGCAATTATAGTGGCAAATCCCACTGACCTTGTTAAAGTTCGACTTCAATCTGAAGG 719
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        666 ATTAGCAATTATAGTGGCAAATCCGACTGACCTTGTTAAAGTTCGACTTCAATCTGAAGG 725

Qy        720 TAAACTCCCCCCTGGGGTACCGAGACGTTATTCAGGGGCGCTAAATGCTTATTCAACCAT 779
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        726 TAAACTCCCCCCTGGGGTACCAAGACGTTATTCAGGGGCGCTAAATGCTTATTCAACCAT 785

Qy        780 AGTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCCCGCAA 839
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Db        786 AGTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCCCGCAA 845

Qy        840 TGCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGACAATCTTAAA 899
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Db        846 TGCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACA---------- 893

Qy        900 ATTACCAGGATTCTCAGATAATATTTTTACTCATATTTTAGCCGGTCTGGGGGCAGGTTT 959
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Db        894 ---------------------------------------------------------- 893

Qy        960 TTTTGCCGTCTGTATCGGTTCTCCTGTTGATGTGATGAAGTCTAGAATGATGGGAGATTC 1019
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Db        894 ----------------------------GATGAAGTCTAGAATGATGGGAGATTC 920

Qy       1020 AGCCTACAAAAGCACATTTGATTGTTTCATCAAGACATTGAAAAATGATGGGCTTCTTGC 1079
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Db        921 AGCCTACAAAAGCACATTTGATTGTTTCATCAAGACGTTGAAAAATGATGGGCCTCTTGC 980

Qy       1080 TTTTTACAAGGGGTTTATCCCAAACTTTGGTCGGTTAGGATCGTGGAATGTGATCATGTT 1139
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Db        981 TTTTTACAAGGGGTTTATCCCAAACTTTGGTCGGTTAGGATCGTGGAATGTGATCATGTT 1040
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Qy       1140 TTTGACCTTGGAGCAGGTCAAGAAGTTTTTCATCAAAGAGGTGCCAAATTAATACATTGA 1199
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Db       1041 TTTGACCTTGGAGCAGGTCAAGAAGTTCTTCATCAAAGAGGTGCCAAATTAATACATTGA 1100

Qy       1200 ACTCGGATAGGAGTAGAAAGAAAGGGTTTTTGTGGAATTTTCTCTACCGGTGTGGATCCT 1259
             | ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1101 AGTCGGATAGGAGTAGAAAAAAAGGGTTTTTGTGGAATTTTCTCTACCGGTGTGGATCCT 1160

Qy       1260 GGCGAGAGACAAATAAATCTTCCTGACTGCTCAGATG-TGTACCTTTTTTATGAATGGTT 1318
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Db       1161 GGCGAGAGA-GAATAAATCTTCCTGACTGCTCAGATGTTGTACCTTTTTTATGAATGGTT 1219

Qy       1319 CTTTTCTTATAGAGGACAGAGAAAAGAAAA-AAAAAATCATTGTCATTTACTCTTTTTCC 1377
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Db       1220 CTTTTCTTATAGAGGACAGAGAAAATAAAAGAAAAATTCATTGTCATGTACTCTTTTTCC 1279

Qy       1378 CCATTTCTGCTGCTAATC----------------------------------------TT 1397
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Db       1280 CCATTTCTGCTGAGTAGCAGCTATACCAAGCAGACTTTGTTGCTTGGCTGCTGCTAATCT 1339

Qy       1398 GGTAGGAGAAGAAAAGTCTTACATTGAGTGATAACGTTGTTCTCTGCATCCATTATTTTT 1457
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Db       1340 TGTAGCTGAAGAAAAGTCTTACATTGAGTGATAACGTTGTTCTCTGCATCCATTATTTTT 1399

Qy       1458 CAGAGATACTATTTGACACATGAAAAGTAATGCACATCAGGTTTTTTTTAAAAAAAAAAA 1517
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Db       1400 CAGAGTTACTATTTGACACATGAAAAGTTTTTTTTTTTTTTTTTTTTTTAACAGGCAGC 1459

Qy       1518 AAAAAAA 1524
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Db       1460 AAATAGA 1466
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RESULT 5
BD011856
LOCUS BD011856 2991 bp DNA linear PAT 02-AUG-2002
DEFINITION Thermogenesis genes and thermogenesis proteins in plant.
ACCESSION BD011856
VERSION BD011856.1 GI:22092045
KEYWORDS WO 0077211-A/2.
SOURCE Symplocarpus foetidus
ORGANISM Symplocarpus foetidus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
REFERENCE 1 (bases 1 to 2991)
AUTHORS Ito,K.
TITLE Thermogenesis genes and thermogenesis proteins in plant
JOURNAL Patent: WO 0077211-A 2 21-DEC-2000;
JAPAN SCIENCE AND TECHNOLOGY CORP,KIKUKATSU ITO
COMMENT OS Symplocarpus foetidus
PN WO 0077211-A/2
PD 21-DEC-2000
PF 12-JUN-2000 WO 2000JP003806
PR 14-JUN-1999 JP 99P 167439
PI KIKUKATSU ITO
PC C12N15/29,C07K14/415
CC

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FT   polyA_site      (1171)
FT   polyA_site      (1176)
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Query Match 70.6%; Score 1076.6; DB 6; Length 2991;
Best Local Similarity 86.6%; Pred. No. 4.4e-263;
Matches 1357; Conservative 0; Mismatches 49; Indels 161; Gaps 9;

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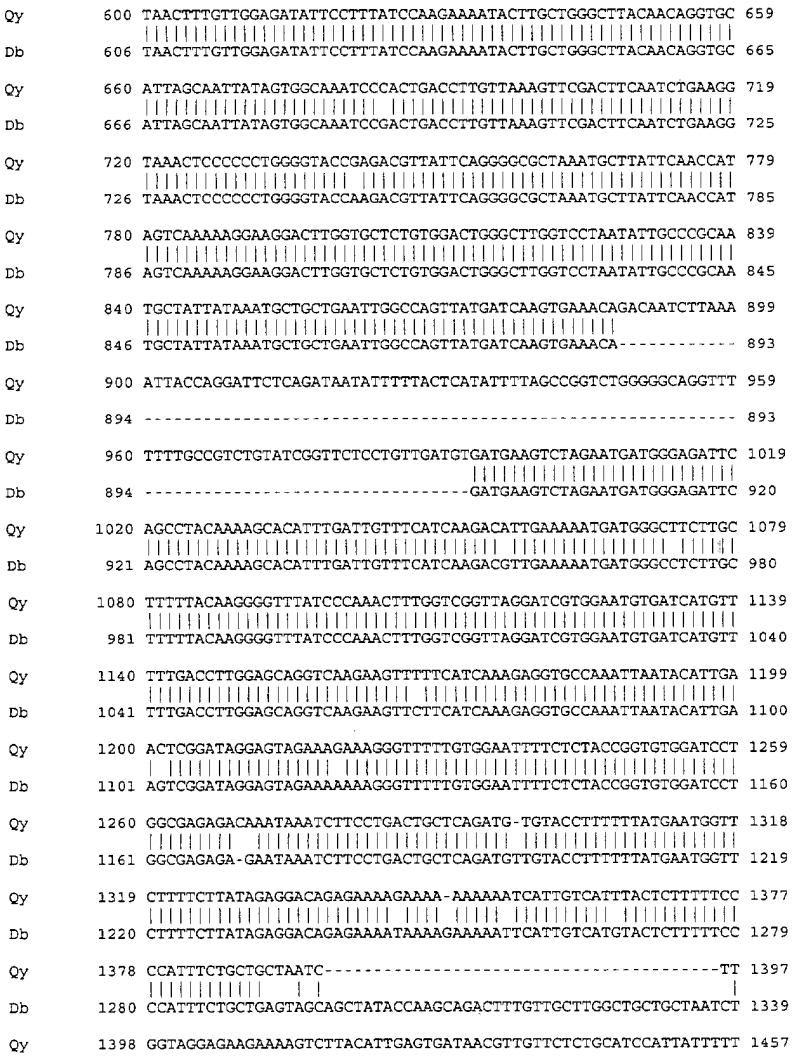
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RESULT 6
AB024734
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DEFINITION  Symplocarpus foetidus mRNA for SfUCPb, complete cds.
ACCESSION   AB024734
VERSION     AB024734.1  GI:7106158
KEYWORDS    .
SOURCE      Symplocarpus foetidus
  ORGANISM  Symplocarpus foetidus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
REFERENCE   1
  AUTHORS   Ito,K.
  TITLE     Isolation of two distinct cold-inducible cDNAs encoding plant
            uncoupling proteins from the spadix of skunk cabbage (Symplocarpus
            foetidus)
  JOURNAL   Plant Sci. 149, 167-173 (1999)
REFERENCE   2  (bases 1 to 2991)
  AUTHORS   Ito,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAR-1999) Kikukatsu Ito, Cryobiosystem Research
            Center, Iwate Univ., Division of Biosystem and Bioresource
            Technology; 3-18-8, Ueda, Morioka 020-8550, Japan
            (E-mail:kikuito@iwate-u.ac.jp, Tel:81-19-621-6253)
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ORIGIN

  Query Match             70.6%;  Score 1076.6;  DB 8;  Length 2991;
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 Best Local Similarity   86.6%;  Pred. No. 4.4e-263;
 Matches 1357;  Conservative    0;  Mismatches   49;  Indels  161;  Gaps    9;

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Db         18 GAGGATTCGCAGAAGAAAGGCCAGAACCCGATTCCTTCCCGTCTTCTTCTCCTTCCGCCC 77

Qy         61 AATTGCAGTTTTTCGCAGCGGCGTCATCATCAAGACCCTCCGCCTTTCCGCGCCAAACGC 120
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Qy        121 CTTCCACCCCCACCCAATCGCCCTCCGTTTCCCGAAATATTCCTCTTCCCTCCTCCCTTT 180
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Qy        840 TGCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGACAATCTTAAA 899
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Db        894 ------------------------------------------------------------ 893

Qy        960 TTTTGCCGTCTGTATCGGTTCTCCTGTTGATGTGATGAAGTCTAGAATGATGGGAGATTC 1019
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Qy       1458 CAGAGATACTATTTGACACATGAAAAGTAATGCACATCAGGTTTTTTTTAAAAAAAAAAA 1517
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Search completed: June  5, 2004, 03:10:28
Job time : 5865.22 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 16:54:52 ; Search time 571.031 Seconds
(without alignments)
11345.276 Million cell updates/sec

Title: US-10-671-628-1
Perfect score: 1525
Sequence: 1 gaggattcgcagaagaaagg.....taaaaaaaaaaaaaaaaaa 1525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
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7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	500.8	32.8	1103	3	AAC46816	Aac46816 Arabidops
6	500.8	32.8	1225	5	AAS14822	Aas14822 Arabidops
7	473	31.0	1088	5	AAS14823	Aas14823 Arabidops
8	473	31.0	1224	3	AAC49402	Aac49402 Arabidops
9	471.4	30.9	1227	3	AAC33096	Aac33096 Arabidops
10	425.6	27.9	957	3	AAC49389	Aac49389 Arabidops
11	422.2	27.7	915	7	ADA70324	Ada70324 Rice gene
12	415.4	27.2	974	5	AAS14825	Aas14825 Wheat cDN
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16	163	10.7	1949	2	AAV71228	Aav71228 cDNA enco
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18	163	10.7	1949	4	AAD09319	Aad09319 Mouse unc
19	160.6	10.5	1204	2	AAV71712	Aav71712 Mouse unc
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21	159	10.4	1215	9	ADB52719	Adb52719 Primary r
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26	156	10.2	930	2	AAX99435	Aax99435 UCP2 Nucl
27	156	10.2	930	6	ABK86151	Abk86151 cDNA enco
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44	152.8	10.0	1888	2	AAX99436	Aax99436 UCP2 nucl
45	152.8	10.0	1888	6	ABK84483	Abk84483 Human cDN

ALIGNMENTS

RESULT 1
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ID AAF77825 standard; cDNA; 1525 BP.
XX
AC AAF77825;
XX
DT 29-MAY-2001 (first entry)
XX
DE SfUCPa derived exothermicity relating gene coding sequence #1.
XX
KW SfUCPa derived exothermicity relating gene; diabetes; obesity;
KW exothermic material; low temperature resistant plant; ss.
XX
OS Symplocarpus foetidus.
XX
PN JP2000354489-A.
XX

PD 26-DEC-2000.
XX
PF 14-JUN-1999; 99JP-00167439.
XX
PR 14-JUN-1999; 99JP-00167439.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2001-260368/27.
DR P-PSDB; AAB73297.
XX
PT Exothermicity relating genes and proteins, useful in the treatment of
PT diabetes and obesity.
XX
PS Claim 1; Page 6-7; 15pp; Japanese.
XX
CC The present sequence is the coding sequence for a Symplocarpus foetidus
CC (SfUCPa) derived exothermicity relating gene. The gene is useful for
CC preparation of low temperature resistant plants, and in the treatment of
CC diabetes and obesity. The encoded protein is useful as exothermic
CC materials for industrial use
XX
SQ Sequence 1525 BP; 398 A; 341 C; 334 G; 452 T; 0 U; 0 Other;

Query Match 100.0%; Score 1525; DB 4; Length 1525;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         61 AATTGCAGTTTTTCGCAGCGGCGTCATCATCAAGACCCTCCGCCTTTCCGCGCCAAACGC 120

Qy        121 CTTCCACCCCCACCCAATCGCCCTCCGTTTCCCGAAATATTCCTCTTCCCTCCTCCCTTT 180
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Qy        361 TGCACGATTCCGTTGGACACTGCTAAAGTTAGGCTTCAACTCCAAAAGAAAGCAGTAACA 420
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Qy        481 AGGGAGGAAGGTTTGTCGGCACTCTGGAAAGGAATTGTACCCGGTTTGCATCGTCAATGC 540
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAACTCCCCCCTGGGGTACCGAGACGTTATTCAGGGGCGCTAAATGCTTATTCAACCATA 780

Qy        781 GTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCCCGCAAT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCCCGCAAT 840

Qy        841 GCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGACAATCTTAAAA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGACAATCTTAAAA 900

Qy        901 TTACCAGGATTCTCAGATAATATTTTTACTCATATTTTAGCCGGTCTGGGGGCAGGTTTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTACCAGGATTCTCAGATAATATTTTTACTCATATTTTAGCCGGTCTGGGGGCAGGTTTT 960

Qy        961 TTTGCCGTCTGTATCGGTTCTCCTGTTGATGTGATGAAGTCTAGAATGATGGGAGATTCA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTTGCCGTCTGTATCGGTTCTCCTGTTGATGTGATGAAGTCTAGAATGATGGGAGATTCA 1020

Qy       1021 GCCTACAAAAGCACATTTGATTGTTTCATCAAGACATTGAAAAATGATGGGCTTCTTGCT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GCCTACAAAAGCACATTTGATTGTTTCATCAAGACATTGAAAAATGATGGGCTTCTTGCT 1080

Qy       1081 TTTTACAAGGGGTTTATCCCAAACTTTGGTCGGTTAGGATCGTGGAATGTGATCATGTTT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TTTTACAAGGGGTTTATCCCAAACTTTGGTCGGTTAGGATCGTGGAATGTGATCATGTTT 1140

Qy       1141 TTGACCTTGGAGCAGGTCAAGAAGTTTTTCATCAAAGAGGTGCCAAATTAATACATTGAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TTGACCTTGGAGCAGGTCAAGAAGTTTTTCATCAAAGAGGTGCCAAATTAATACATTGAA 1200

Qy       1201 CTCGGATAGGAGTAGAAAGAAAGGGTTTTTGTGGAATTTTCTCTACCGGTGTGGATCCTG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 CTCGGATAGGAGTAGAAAGAAAGGGTTTTTGTGGAATTTTCTCTACCGGTGTGGATCCTG 1260

Qy       1261 GCGAGAGACAAATAAATCTTCCTGACTGCTCAGATGTGTACCTTTTTTATGAATGGTTCT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

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Db       1261 GCGAGAGACAAATAAATCTTCCTGACTGCTCAGATGTGTACCTTTTTTATGAATGGTTCT 1320

Qy       1321 TTTCTTATAGAGGACAGAGAAAAGAAAAAAAAAATCATTGTCATTTACTCTTTTTCCCCA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TTTCTTATAGAGGACAGAGAAAAGAAAAAAAAAATCATTGTCATTTACTCTTTTTCCCCA 1380

Qy       1381 TTTCTGCTGCTAATCTTGGTAGGAGAAGAAAAGTCTTACATTGAGTGATAACGTTGTTCT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTCTGCTGCTAATCTTGGTAGGAGAAGAAAAGTCTTACATTGAGTGATAACGTTGTTCT 1440

Qy       1441 CTGCATCCATTATTTTTCAGAGATACTATTTGACACATGAAAAGTAATGCACATCAGGTT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 CTGCATCCATTATTTTTCAGAGATACTATTTGACACATGAAAAGTAATGCACATCAGGTT 1500

Qy       1501 TTTTTTAAAAAAAAAAAAAAAAAAA 1525
              |||||||||||||||||||||||||
Db       1501 TTTTTTAAAAAAAAAAAAAAAAAAA 1525
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Search completed: June 4, 2004, 22:21:07
Job time : 576.031 secs

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 21:05:07 ; Search time 3860.45 Seconds
(without alignments)
11796.502 Million cell updates/sec

Title: US-10-671-628-1
Perfect score: 1525
Sequence: 1 gaggattcgcagaagaaagg.....taaaaaaaaaaaaaaaaaa 1525

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Search completed: June 5, 2004, 06:21:11
Job time : 3866.45 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		540.4	35.4	1241	14	CB330501	CB330501 SpEST485
2		516.2	33.8	871	14	CB290646	CB290646 UCRCS01_0
3		446.6	29.3	1447	13	BU103700	BU103700 SCEPAM201
4		443	29.0	797	13	BQ743348	BQ743348 WHE4102_H
5		437.2	28.7	1422	11	AY105357	AY105357 Zea mays
6		429.2	28.1	779	14	CF448435	CF448435 EST684780
7		425.8	27.9	746	14	CF089986	CF089986 QHM3D13.y
8		425	27.9	660	12	BI096046	BI096046 PIP2ER_E1
9		423.2	27.8	878	14	CD433462	CD433462 EL01N0308
10		404.2	26.5	712	14	CF452690	CF452690 EST689035
11		403.6	26.5	719	14	CF445646	CF445646 EST681991
c 12		397	26.0	894	14	CB290645	CB290645 UCRCS01_0
13		396.4	26.0	1085	14	CK207934	CK207934 FGAS01960
14		394	25.8	762	14	CF213174	CF213174 CGF100063
15		391.4	25.7	746	14	CD921168	CD921168 G608.119K
16		390.8	25.6	832	10	BE642116	BE642116 Cri2_5_D0
17		390.6	25.6	742	14	CB648044	CB648044 OSJNEb11E
18		388	25.4	670	9	AJ432683	AJ432683 AJ432683
19		386.2	25.3	733	13	BQ972958	BQ972958 QHI11G22.
20		376.8	24.7	670	14	CF810597	CF810597 CA297F cD
21		373	24.5	695	14	CB648002	CB648002 OSJNEb11D
22		367.2	24.1	756	13	CA086808	CA086808 SCQGAM202
23		367	24.1	682	14	CF436214	CF436214 EST672559
24		361.6	23.7	649	14	CF442797	CF442797 EST679142
25		360.8	23.7	768	12	BG321351	BG321351 Ds01_07d1
26		357	23.4	610	13	BQ967986	BQ967986 QHB32H05.
27		355.8	23.3	872	12	BG446588	BG446588 GA__Eb003
28		353.6	23.2	766	13	BQ483475	BQ483475 WHE3509_A
c 29		352	23.1	1153	14	CK209055	CK209055 FGAS02079
30		341.6	22.4	994	12	BG416382	BG416382 HVSMEk001
31		337.2	22.1	747	14	CD841700	CD841700 RFO2.124F
32		337	22.1	817	14	CD447945	CD447945 EL01N0202
33		333	21.8	821	10	BE641808	BE641808 Cri2_4_F0
34		332	21.8	679	12	BG450507	BG450507 NF019G07D
35		331.4	21.7	598	13	BQ916601	BQ916601 QHB18H04.
36		329.8	21.6	769	14	CD829664	CD829664 BN40.042N
c 37		329	21.6	714	12	BJ283810	BJ283810 BJ283810
38		326.2	21.4	603	10	BF727999	BF727999 1000057C0
39		325.2	21.3	692	13	BQ969842	BQ969842 QHB39L02.
40		324.6	21.3	628	10	AW330667	AW330667 707032G04
41		324.6	21.3	643	14	CA271689	CA271689 SCMCLB208
42		323.8	21.2	506	13	BQ106121	BQ106121 gg0398.e
43		322	21.1	678	13	BQ909270	BQ909270 QHA10A22.
44		322	21.1	709	13	BQ842169	BQ842169 WHE2989_F
45		319.4	20.9	798	14	CD433355	CD433355 EL01N0307

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 16:59:57 ; Search time 11489.8 Seconds
(without alignments)
11282.980 Million cell updates/sec

Title: US-10-671-628-3
Perfect score: 2991
Sequence: 1 tggtggtgacgagtgacgag.....ccagccagtaaaaaaaaaaa 2991

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2991	100.0	2991	6	E50744	E50744 Plant exoth
	2	2991	100.0	2991	6	BD011856	BD011856 Thermogen
	3	2991	100.0	2991	8	AB024734	AB024734 Symplocar
	4	1076.6	36.0	1525	6	E50743	E50743 Plant exoth
	5	1076.6	36.0	1525	6	BD011855	BD011855 Thermogen
	6	1076.6	36.0	1525	8	AB024733	AB024733 Symplocar
	7	456.8	15.3	1209	8	AB088762	AB088762 Helicodic
	8	374.6	12.5	1429	8	AF472619	AF472619 Lycopersi
	9	368.2	12.3	1434	8	STUCPMRNA	Y11220 Solanum tub
	10	347.4	11.6	920	6	AX651736	AX651736 Sequence
	11	347.4	11.6	921	6	AX506066	AX506066 Sequence
	12	347.4	11.6	921	8	AF146226	AF146226 Arabidops
	13	347.4	11.6	952	8	AY091185	AY091185 Arabidops
	14	347.4	11.6	1274	8	AY056272	AY056272 Arabidops
	15	339.4	11.3	1240	8	ATMTUNCOU	AJ001264 Arabidops
	16	337.8	11.3	1225	6	AX269361	AX269361 Sequence
	17	337.8	11.3	1225	8	ATPUMP	AJ223983 Arabidops
	18	320.4	10.7	1088	6	AX269362	AX269362 Sequence
	19	320.4	10.7	1088	8	AB021706	AB021706 Arabidops
	20	318.8	10.7	1227	8	AY088200	AY088200 Arabidops
	21	310	10.4	1376	8	BT009306	BT009306 Triticum
	22	273.2	9.1	1243	8	AF461732	AF461732.Zea mays
	23	272.8	9.1	1263	8	AK061318	AK061318 Oryza sat
	24	271.2	9.1	1179	8	AK104090	AK104090 Oryza sat
	25	251.8	8.4	915	6	AX653777	AX653777 Sequence
	26	241.8	8.1	974	6	AX269364	AX269364 Sequence
	27	241.8	8.1	974	8	AB042428	AB042428 Triticum
	28	238.6	8.0	971	8	AB042429	AB042429 Triticum
	29	178.4	6.0	1405	8	AK102326	AK102326 Oryza sat
	30	178.4	6.0	1451	8	AK103874	AK103874 Oryza sat
	31	156.8	5.2	825	6	AX652954	AX652954 Sequence
c	32	156.2	5.2	1703	8	AY251055	AY251055 Anthurium
c	33	153.2	5.1	1157	8	AF343446	AF343446 Actinidia
c	34	150	5.0	777	8	ACTACTB	M21336 Actinidia d

c	35	150	5.0	809	8	ACACT7	X13139 Actinidia c
c	36	150	5.0	1370	8	ACTINID	X16466 Actinidia d
c	37	149.6	5.0	1361	8	VSCYSPRO	X75749 V.sativa L.
c	38	146.8	4.9	1137	8	ACTACTA	M21335 Actinidia d
c	39	146.8	4.9	1138	8	ACACT1	X13013 Actinidia c
c	40	143.4	4.8	1830	8	AF019147	AF019147 Zea mays
c	41	142	4.7	1751	8	AF259983	AF259983 Ipomoea b
c	42	141.6	4.7	1699	8	AF454957	AF454957 Brassica
	43	140.6	4.7	6428	6	AX269360	AX269360 Sequence
	44	140.6	4.7	6428	8	STAJ2586	AJ002586 Solanum t
c	45	138.6	4.6	1828	8	AB020961	AB020961 Zea mays

ALIGNMENTS

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RESULT 1
E50744
LOCUS       E50744                  2991 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Plant exotherm-related gene and exotherm-related protein.
ACCESSION   E50744
VERSION     E50744.1  GI:18622140
KEYWORDS    JP 2000354489-A/2.
SOURCE      Symplocarpus foetidus
  ORGANISM  Symplocarpus foetidus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
REFERENCE   1  (bases 1 to 2991)
  AUTHORS   Ito,K.
  TITLE     Plant exotherm-related gene and exotherm-related protein
  JOURNAL   Patent: JP 2000354489-A 2 26-DEC-2000;
            SCIENCE & TECH AGENCY
COMMENT     OS   Symplocarpus foetidus
            PN   JP 2000354489-A/2
            PD   26-DEC-2000
            PF   14-JUN-1999 JP 1999167439
            PR
            PI   KIKUICHI ITO
            PC   C12N15/09,C07K14/415//A01H5/00,A61K31/00,A61K31/00,A61K38/00,
            PC   C12P21/02,
            PC   C12N15/00,A61K37/02
            CC
            FH   Key             Location/Qualifiers
            FT   CDS             (286). .(1089)
            FT   polyA_site      (1171). .(1176)
            FT   polyA_site      (1243). .(1248).
FEATURES             Location/Qualifiers
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                     /organism="Symplocarpus foetidus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:28477"
ORIGIN

  Query Match           100.0%;  Score 2991;  DB 6;  Length 2991;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 2991;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TGGTGGTGACGAGTGACGAGGATTCGCAGAAGAAAGGCCAGAACCCGATTCCTTCCCGTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGGTGGTGACGAGTGACGAGGATTCGCAGAAGAAAGGCCAGAACCCGATTCCTTCCCGTC 60

Qy         61 TTCTTCTCCTTCCGCCCAATTGCAGTTTTTCGCAGCGGGTCATCATCAAGACCCTCCGCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TTCTTCTCCTTCCGCCCAATTGCAGTTTTTCGCAGCGGGTCATCATCAAGACCCTCCGCC 120

Qy        121 TTTCCGCGCCAAACGCCTTCCACCCAATCCCTCCGTTTCCCGAAATATTCCCCTTCCCTC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TTTCCGCGCCAAACGCCTTCCACCCAATCCCTCCGTTTCCCGAAATATTCCCCTTCCCTC 180

Qy        181 CCTTTTCTTCTCTACATAAACCCTAACCACCCCCATCCTCTCCTCCCGCTTCCGACCACC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCTTTTCTTCTCTACATAAACCCTAACCACCCCCATCCTCTCCTCCCGCTTCCGACCACC 240

Qy        241 CTGCATTCTACTGGGATCCCATTTGATCGACGTTTCCCGGCGAGGATGGGCGATCACGGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCATTCTACTGGGATCCCATTTGATCGACGTTTCCCGGCGAGGATGGGCGATCACGGC 300

Qy        301 CCGAGGACCGAGATCTCGTTTGCCGGCAGTTCGCGAGCAGCATTCGCCGCTTGCTTCGCC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        361 GAGCTCTGTACGATTCCGTTGGACACTGCTAAAGTTAGGCTTCAGCTCCAAAAGAAAGCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCTCTGTACGATTCCGTTGGACACTGCTAAAGTTAGGCTTCAGCTCCAAAAGAAAGCA 420

Qy        421 GTAACAGGTGATGTGGTGGCTTTGCCAAAATACAGGGGAATGTTGGGCACTGTTGCCACT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTAACAGGTGATGTGGTGGCTTTGCCAAAATACAGGGGAATGTTGGGCACTGTTGCCACT 480

Qy        481 ATTGCCAGGGAGGAAGGTTTGTCGGCACTCTGGAAAGGAATTGTACCCGGTTTGCATCGT 540
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Db        481 ATTGCCAGGGAGGAAGGTTTGTCGGCACTCTGGAAAGGAATTGTACCCGGTTTGCATCGT 540

Qy        541 CAATGCCTCTTTGGAGGGCTACGAATTGGGTTGTATGAACCAGTTAAGTCCTTTTATGTT 600
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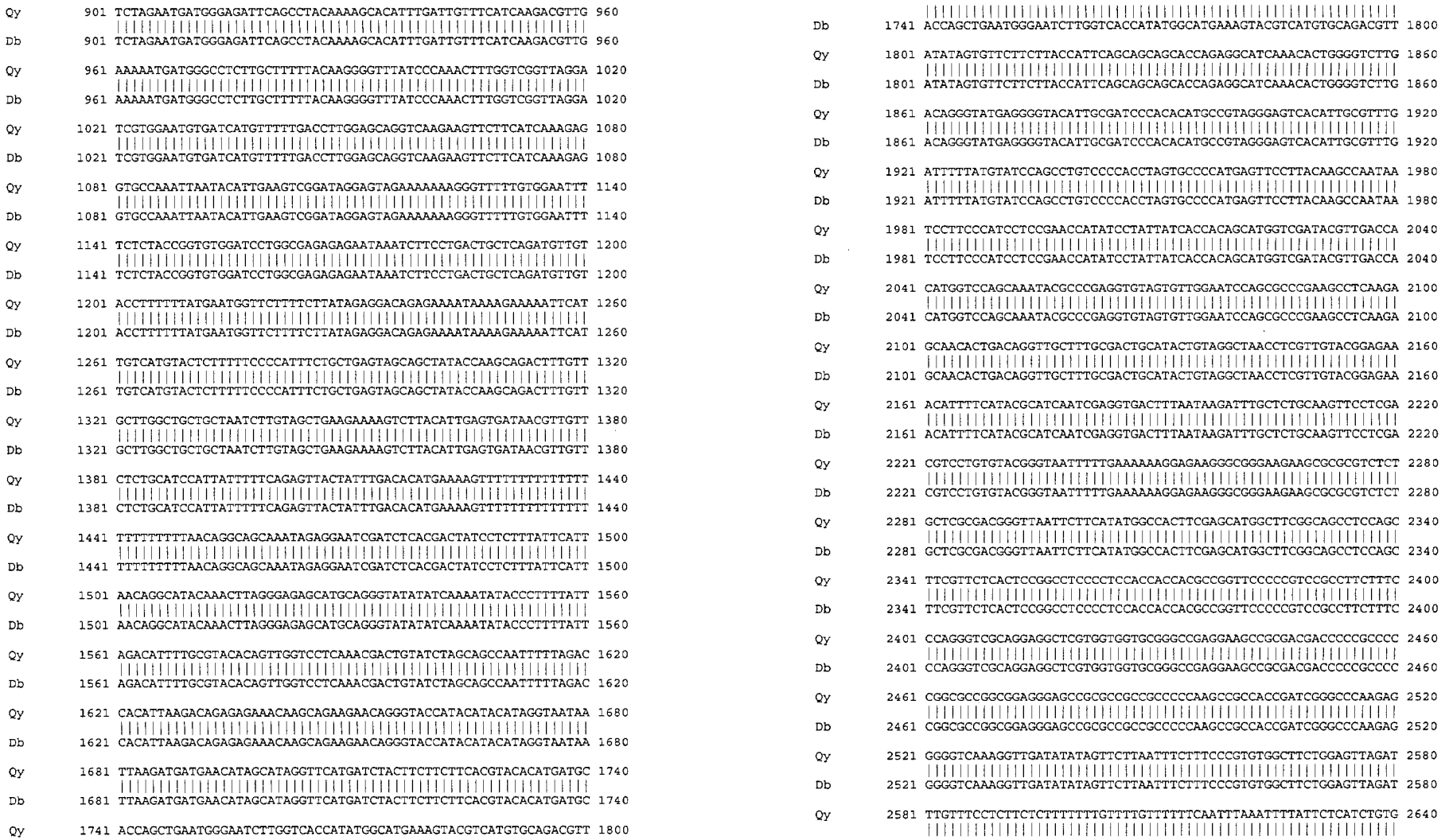
Qy        601 GGAGATAACTTTGTTGGAGATATTCCTTTATCCAAGAAAATACTTGCTGGGCTTACAACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGAGATAACTTTGTTGGAGATATTCCTTTATCCAAGAAAATACTTGCTGGGCTTACAACA 660

Qy        661 GGTGCATTAGCAATTATAGTGGCAAATCCGACTGACCTTGTTAAAGTTCGACTTCAATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGTGCATTAGCAATTATAGTGGCAAATCCGACTGACCTTGTTAAAGTTCGACTTCAATCT 720

Qy        721 GAAGGTAAACTCCCCCCTGGGGTACCAAGACGTTATTCAGGGGCGCTAAATGCTTATTCA 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAGGTAAACTCCCCCCTGGGGTACCAAGACGTTATTCAGGGGCGCTAAATGCTTATTCA 780

Qy        781 ACCATAGTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACCATAGTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCC 840

Qy        841 CGCAATGCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGATGAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCAATGCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGATGAAG 900
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Db       2581 TTGTTTCCTCTTCTCTTTTTTTGTTTTGTTTTTTCAATTTAAATTTTATTCTCATCTGTG 2640

Qy       2641 GACGACCTTCCATCGGGGTTTTCGTCCCTCTCGCAGGTGAAGATCTCCGGAAGGAATCCT 2700
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       2701 ACTGGTTCAACGGTGTCGGATCGGTGGTGGCTGTTGATCAGGATCCGGCGACTCGATACC 2760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 ACTGGTTCAACGGTGTCGGATCGGTGGTGGCTGTTGATCAGGATCCGGCGACTCGATACC 2760

Qy       2761 CGGTCGTGGTTCGGTTCACCAAGGTCAACTATGCGAACGTCTCGACCAACAACTACGCAC 2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2761 CGGTCGTGGTTCGGTTCACCAAGGTCAACTATGCGAACGTCTCGACCAACAACTACGCAC 2820

Qy       2821 TGGACGAGATCCTGGAGGTGAAATGAGGGTCGGCGGGCGTGGTCGGTCGGGCATGTCACG 2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 TGGACGAGATCCTGGAGGTGAAATGAGGGTCGGCGGGCGTGGTCGGTCGGGCATGTCACG 2880

Qy       2881 ATGATGTATTTTCGCAGTTGGTAGTGTAAAATACCATGTCATTCGTGTAAAACTCTTTCG 2940
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Qy       2941 TTCGCCAAATCCTCAGTTGAAATTTTAATTCCCAGCCAGTAAAAAAAAAAA 2991
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RESULT 2
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DEFINITION  Thermogenesis genes and thermogenesis proteins in plant.
ACCESSION   BD011856
VERSION     BD011856.1  GI:22092045
KEYWORDS    WO 0077211-A/2.
SOURCE      Symplocarpus foetidus
  ORGANISM  Symplocarpus foetidus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Araceae; Symplocarpus.
REFERENCE   1  (bases 1 to 2991)
  AUTHORS   Ito,K.
  TITLE     Thermogenesis genes and thermogenesis proteins in plant
  JOURNAL   Patent: WO 0077211-A 2 21-DEC-2000;
            JAPAN SCIENCE AND TECHNOLOGY CORP,KIKUKATSU ITO
COMMENT     OS   Symplocarpus foetidus
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            PD   21-DEC-2000
            PF   12-JUN-2000 WO 2000JP003806
            PR   14-JUN-1999 JP 99P   167439
            PI   KIKUKATSU ITO
            PC   C12N15/29,C07K14/415
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Qy         61 TTCTTCTCCTTCCGCCCAATTGCAGTTTTTCGCAGCGGGTCATCATCAAGACCCTCCGCC 120
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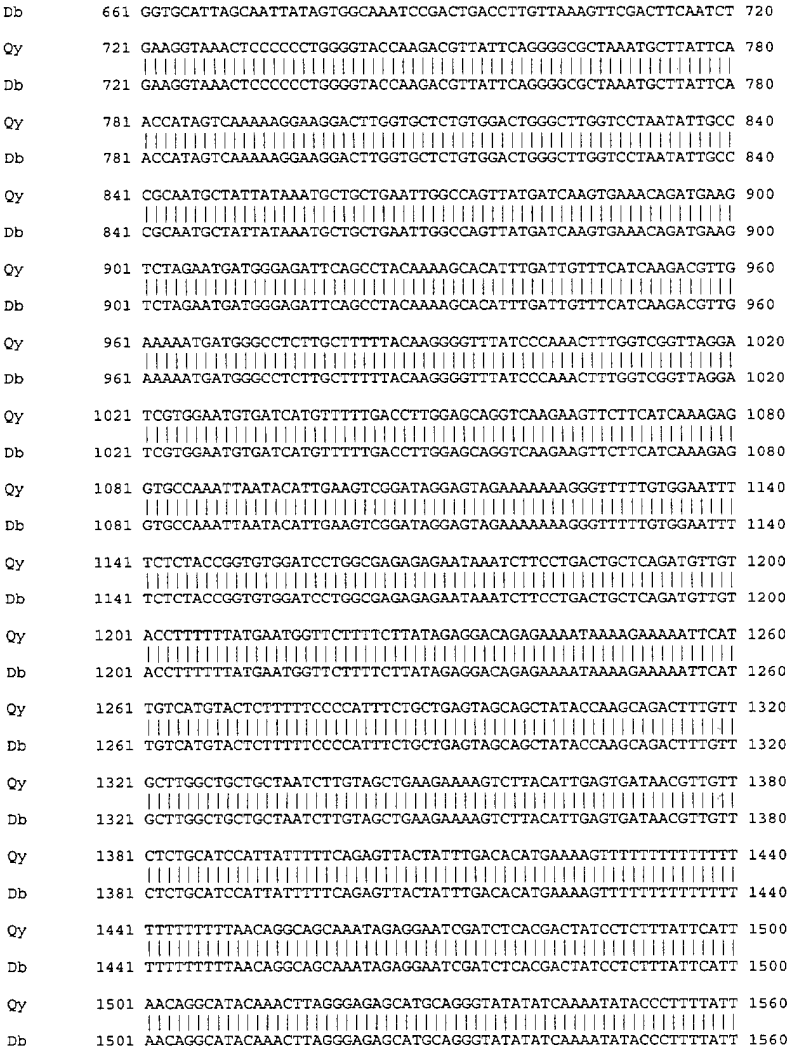
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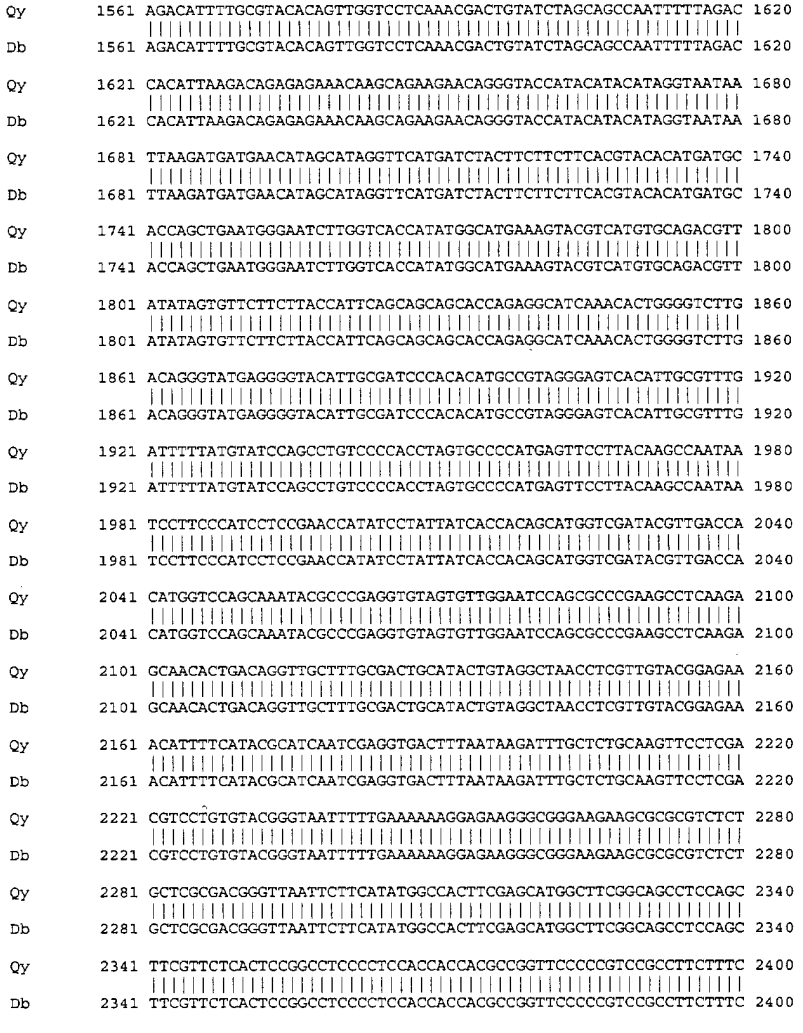
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Db 961 AAAAATGATGGGCCTCTTGCTTTTTACAAGGGGTTTATCCCAAACTTTGGTCGGTTAGGA 1020
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Qy       2701 ACTGGTTCAACGGTGTCGGATCGGTGGTGGCTGTTGATCAGGATCCGGCGACTCGATACC 2760
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RESULT 3
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DEFINITION  Symplocarpus foetidus mRNA for SfUCPb, complete cds.
ACCESSION   AB024734
VERSION     AB024734.1  GI:7106158
KEYWORDS    .
SOURCE      Symplocarpus foetidus
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REFERENCE   1
  AUTHORS   Ito,K.
  TITLE     Isolation of two distinct cold-inducible cDNAs encoding plant
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  JOURNAL   Plant Sci. 149, 167-173 (1999)
REFERENCE   2  (bases 1 to 2991)
  AUTHORS   Ito,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAR-1999) Kikukatsu Ito, Cryobiosystem Research
            Center, Iwate Univ., Division of Biosystem and Bioresource
            Technology; 3-18-8, Ueda, Morioka 020-8550, Japan
            (E-mail:kikuito@iwate-u.ac.jp, Tel:81-19-621-6253)
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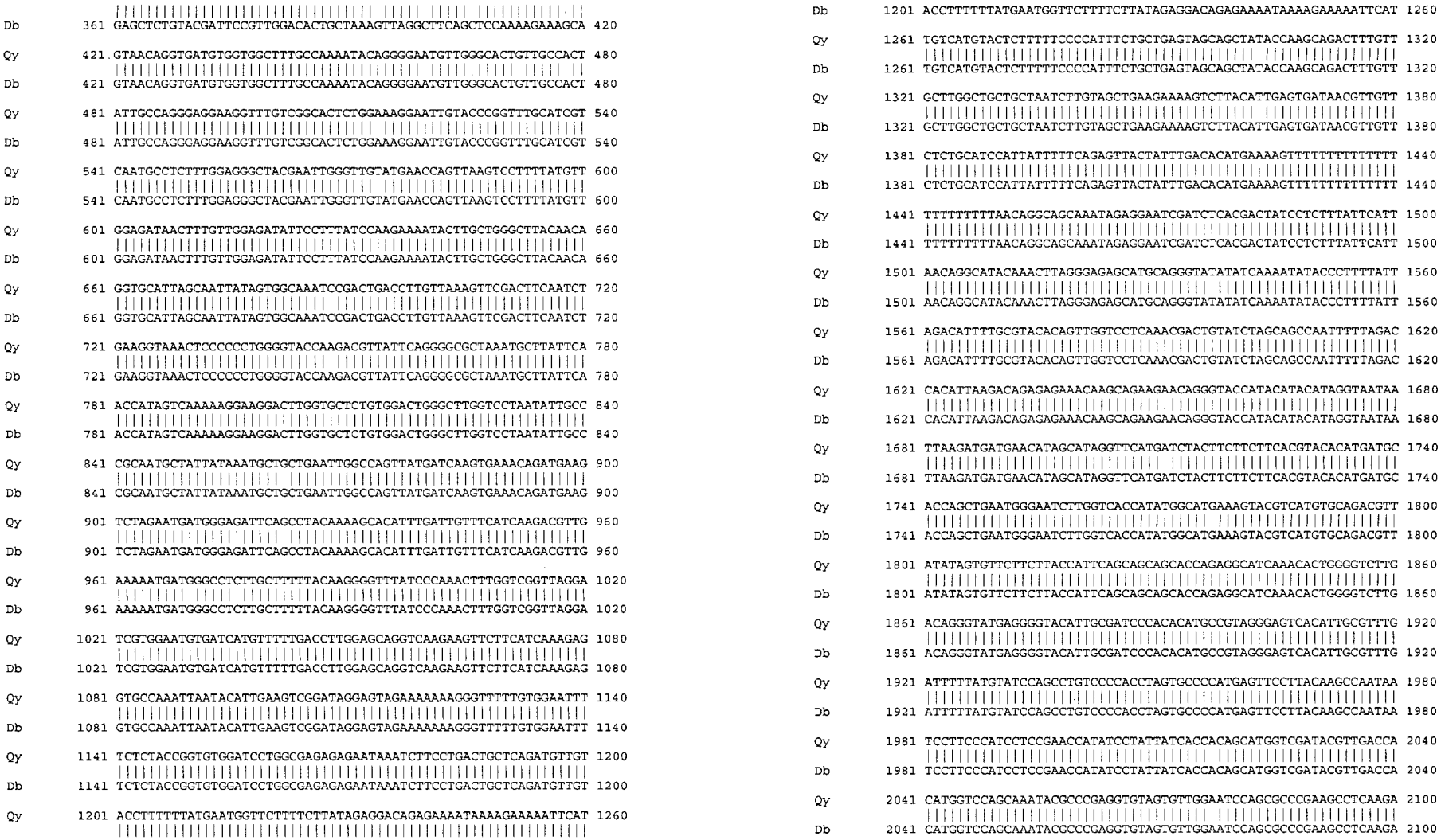
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Db 1501 AACAGGCATACAAACTTAGGGAGAGCATGCAGGGTATATATCAAAATATACCCTTTTATT 1560
Qy 1561 AGACATTTTGCGTACACAGTTGGTCCTCAAACGACTGTATCTAGCAGCCAATTTTTAGAC 1620
Db 1561 AGACATTTTGCGTACACAGTTGGTCCTCAAACGACTGTATCTAGCAGCCAATTTTTAGAC 1620
Qy 1621 CACATTAAGACAGAGAGAAACAAGCAGAAGAACAGGGTACCATACATACATAGGTAATAA 1680
Db 1621 CACATTAAGACAGAGAGAAACAAGCAGAAGAACAGGGTACCATACATACATAGGTAATAA 1680
Qy 1681 TTAAGATGATGAACATAGCATAGGTTCATGATCTACTTCTTCTTCACGTACACATGATGC 1740
Db 1681 TTAAGATGATGAACATAGCATAGGTTCATGATCTACTTCTTCTTCACGTACACATGATGC 1740
Qy 1741 ACCAGCTGAATGGGAATCTTGGTCACCATATGGCATGAAAGTACGTCATGTGCAGACGTT 1800
Db 1741 ACCAGCTGAATGGGAATCTTGGTCACCATATGGCATGAAAGTACGTCATGTGCAGACGTT 1800
Qy 1801 ATATAGTGTTCTTCTTACCATTCAGCAGCAGCACCAGAGGCATCAAACACTGGGGTCTTG 1860
Db 1801 ATATAGTGTTCTTCTTACCATTCAGCAGCAGCACCAGAGGCATCAAACACTGGGGTCTTG 1860
Qy 1861 ACAGGGTATGAGGGGTACATTGCGATCCCACACATGCCGTAGGGAGTCACATTGCGTTTG 1920
Db 1861 ACAGGGTATGAGGGGTACATTGCGATCCCACACATGCCGTAGGGAGTCACATTGCGTTTG 1920
Qy 1921 ATTTTTATGTATCCAGCCTGTCCCCACCTAGTGCCCCATGAGTTCCTTACAAGCCAATAA 1980
Db 1921 ATTTTTATGTATCCAGCCTGTCCCCACCTAGTGCCCCATGAGTTCCTTACAAGCCAATAA 1980
Qy 1981 TCCTTCCCATCCTCCGAACCATATCCTATTATCACCACAGCATGGTCGATACGTTGACCA 2040
Db 1981 TCCTTCCCATCCTCCGAACCATATCCTATTATCACCACAGCATGGTCGATACGTTGACCA 2040
Qy 2041 CATGGTCCAGCAAATACGCCCGAGGTGTAGTGTTGGAATCCAGCGCCCGAAGCCTCAAGA 2100
Db 2041 CATGGTCCAGCAAATACGCCCGAGGTGTAGTGTTGGAATCCAGCGCCCGAAGCCTCAAGA 2100

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Qy       2101 GCAACACTGACAGGTTGCTTTGCGACTGCATACTGTAGGCTAACCTCGTTGTACGGAGAA 2160
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Db       2101 GCAACACTGACAGGTTGCTTTGCGACTGCATACTGTAGGCTAACCTCGTTGTACGGAGAA 2160

Qy       2161 ACATTTTCATACGCATCAATCGAGGTGACTTTAATAAGATTTGCTCTGCAAGTTCCTCGA 2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2161 ACATTTTCATACGCATCAATCGAGGTGACTTTAATAAGATTTGCTCTGCAAGTTCCTCGA 2220

Qy       2221 CGTCCTGTGTACGGGTAATTTTTGAAAAAAGGAGAAGGGCGGGAAGAAGCGCGCGTCTCT 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2221 CGTCCTGTGTACGGGTAATTTTTGAAAAAAGGAGAAGGGCGGGAAGAAGCGCGCGTCTCT 2280

Qy       2281 GCTCGCGACGGGTTAATTCTTCATATGGCCACTTCGAGCATGGCTTCGGCAGCCTCCAGC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2281 GCTCGCGACGGGTTAATTCTTCATATGGCCACTTCGAGCATGGCTTCGGCAGCCTCCAGC 2340

Qy       2341 TTCGTTCTCACTCCGGCCTCCCCTCCACCACCACGCCGGTTCCCCCGTCCGCCTTCTTTC 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2341 TTCGTTCTCACTCCGGCCTCCCCTCCACCACCACGCCGGTTCCCCCGTCCGCCTTCTTTC 2400

Qy       2401 CCAGGGTCGCAGGAGGCTCGTGGTGGTGCGGGCCGAGGAAGCCGCGACGACCCCCGCCCC 2460
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Db       2401 CCAGGGTCGCAGGAGGCTCGTGGTGGTGCGGGCCGAGGAAGCCGCGACGACCCCCGCCCC 2460

Qy       2461 CGGCGCCGGCGGAGGGAGCCGCGCCGCCGCCCCCAAGCCGCCACCGATCGGGCCCAAGAG 2520
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Db       2461 CGGCGCCGGCGGAGGGAGCCGCGCCGCCGCCCCCAAGCCGCCACCGATCGGGCCCAAGAG 2520

Qy       2521 GGGGTCAAAGGTTGATATATAGTTCTTAATTTCTTTCCCGTGTGGCTTCTGGAGTTAGAT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2521 GGGGTCAAAGGTTGATATATAGTTCTTAATTTCTTTCCCGTGTGGCTTCTGGAGTTAGAT 2580

Qy       2581 TTGTTTCCTCTTCTCTTTTTTTGTTTTGTTTTTTCAATTTAAATTTTATTCTCATCTGTG 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2581 TTGTTTCCTCTTCTCTTTTTTTGTTTTGTTTTTTCAATTTAAATTTTATTCTCATCTGTG 2640

Qy       2641 GACGACCTTCCATCGGGGTTTTCGTCCCTCTCGCAGGTGAAGATCTCCGGAAGGAATCCT 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2641 GACGACCTTCCATCGGGGTTTTCGTCCCTCTCGCAGGTGAAGATCTCCGGAAGGAATCCT 2700

Qy       2701 ACTGGTTCAACGGTGTCGGATCGGTGGTGGCTGTTGATCAGGATCCGGCGACTCGATACC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2701 ACTGGTTCAACGGTGTCGGATCGGTGGTGGCTGTTGATCAGGATCCGGCGACTCGATACC 2760

Qy       2761 CGGTCGTGGTTCGGTTCACCAAGGTCAACTATGCGAACGTCTCGACCAACAACTACGCAC 2820
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Db       2761 CGGTCGTGGTTCGGTTCACCAAGGTCAACTATGCGAACGTCTCGACCAACAACTACGCAC 2820

Qy       2821 TGGACGAGATCCTGGAGGTGAAATGAGGGTCGGCGGGCGTGGTCGGTCGGGCATGTCACG 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 TGGACGAGATCCTGGAGGTGAAATGAGGGTCGGCGGGCGTGGTCGGTCGGGCATGTCACG 2880

Qy       2881 ATGATGTATTTTCGCAGTTGGTAGTGTAAAATACCATGTCATTCGTGTAAAACTCTTTCG 2940
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Db       2881 ATGATGTATTTTCGCAGTTGGTAGTGTAAAATACCATGTCATTCGTGTAAAACTCTTTCG 2940
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Qy       2941 TTCGCCAAATCCTCAGTTGAAATTTTAATTCCCAGCCAGTAAAAAAAAAAA 2991
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Db       2941 TTCGCCAAATCCTCAGTTGAAATTTTAATTCCCAGCCAGTAAAAAAAAAAA 2991
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Search completed: June 5, 2004, 03:10:32
Job time : 11493.8 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 16:54:52 ; Search time 1119.97 Seconds
(without alignments)
11345.276 Million cell updates/sec

Title: US-10-671-628-3
Perfect score: 2991
Sequence: 1 tggtggtgacgagtgacgag.....ccagccagtaaaaaaaaaaa 2991

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2991	100.0	2991	4	AAF77826	Aaf77826 SfUCPa de
2	1076.6	36.0	1525	4	AAF77825	Aaf77825 SfUCPa de
3	347.4	11.6	920	7	ADA68518	Ada68518 Arabidops
4	347.4	11.6	921	6	ABZ12956	Abz12956 Arabidops
5	347.4	11.6	1103	3	AAC46816	Aac46816 Arabidops
6	337.8	11.3	1225	5	AAS14822	Aas14822 Arabidops
7	320.4	10.7	957	3	AAC49389	Aac49389 Arabidops
8	320.4	10.7	1088	5	AAS14823	Aas14823 Arabidops
9	320.4	10.7	1224	3	AAC49402	Aac49402 Arabidops
10	318.8	10.7	1227	3	AAC33096	Aac33096 Arabidops
11	251.8	8.4	915	7	ADA70324	Ada70324 Rice gene
12	241.8	8.1	974	5	AAS14825	Aas14825 Wheat cDN
13	167.4	5.6	471	3	AAC36817	Aac36817 Arabidops
14	156.8	5.2	825	7	ADA69501	Ada69501 Rice gene
c 15	141.8	4.7	1879	3	AAC44552	Aac44552 Zea mays
16	140.6	4.7	6428	5	AAS14821	Aas14821 S. tubero
17	138.2	4.6	282	6	ABL76423	Abl76423 Corn tass
c 18	137.8	4.6	1645	2	AAV82458	Aav82458 Triticum
c 19	136.2	4.6	1202	8	ADA48993	Ada48993 Wheat gen
c 20	136.2	4.6	1392	6	ABZ13567	Abz13567 Arabidops
c 21	134.8	4.5	1407	8	ADA49223	Ada49223 Maize gen
c 22	133.2	4.5	1056	2	AAT79546	Aat79546 Glycine m
c 23	131.6	4.4	1056	2	AAT74043	Aat74043 Soybean t
c 24	131.6	4.4	1392	6	ABN83213	Abn83213 Soybean D
c 25	131.6	4.4	1392	7	AAL50308	Aal50308 Soybean t
c 26	131.6	4.4	1849	2	AAT74042	Aat74042 Soybean t
c 27	130	4.3	1807	2	AAT74041	Aat74041 Soybean t
28	129.8	4.3	816	6	ABQ93892	Abq93892 Human unc
c 29	129	4.3	1463	4	AAF44787	Aaf44787 Cysteine
c 30	129	4.3	1463	9	ADB94728	Adb94728 Programme
c 31	128.6	4.3	1017	2	AAT68956	Aat68956 Blackcurr
c 32	127.4	4.3	1600	4	AAF44793	Aaf44793 Cysteine
c 33	127.4	4.3	1600	9	ADB94734	Adb94734 Programme
c 34	126.4	4.2	1474	2	AAT90174	Aat90174 Oil seed
c 35	126.2	4.2	557	4	AAF44798	Aaf44798 Cysteine
c 36	126.2	4.2	557	9	ADB94739	Adb94739 Programme
c 37	126.2	4.2	1390	2	AAT90171	Aat90171 Oil seed
c 38	126.2	4.2	1434	2	AAT90172	Aat90172 Oil seed
c 39	126.2	4.2	1441	2	AAT90173	Aat90173 Oil seed
c 40	126.2	4.2	1776	9	ADB94872	Adb94872 Programme
c 41	125.8	4.2	886	4	AAF44789	Aaf44789 Cysteine
c 42	125.8	4.2	886	9	ADB94730	Adb94730 Programme
c 43	124	4.1	1317	7	ADA70847	Ada70847 Rice gene
c 44	124	4.1	1317	8	ADA48729	Ada48729 Rice gene
c 45	123.6	4.1	910	2	AAV66759	Aav66759 Pathogen

ALIGNMENTS

RESULT 1
AAF77826
ID AAF77826 standard; cDNA; 2991 BP.
XX
AC AAF77826;
XX
DT 29-MAY-2001 (first entry)
XX
DE SfUCPa derived exothermicity relating gene coding sequence #2.
XX
KW SfUCPa derived exothermicity relating gene; diabetes; obesity;
KW exothermic material; low temperature resistant plant; ss.
XX
OS Symplocarpus foetidus.
XX
PN JP2000354489-A.
XX
PD 26-DEC-2000.

XX

PF 14-JUN-1999; 99JP-00167439.

XX

PR 14-JUN-1999; 99JP-00167439.

XX

PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

XX

DR WPI; 2001-260368/27.

DR P-PSDB; AAB73298.

XX

PT Exothermicity relating genes and proteins, useful in the treatment of
PT diabetes and obesity.

XX

PS Claim 2; Page 8-10; 15pp; Japanese.

XX

CC The present sequence is the coding sequence for a Symplocarpus foetidus
CC (SfUCPa) derived exothermicity relating gene. The gene is useful for
CC preparation of low temperature resistant plants, and in the treatment of
CC diabetes and obesity. The encoded protein is useful as exothermic
CC materials for industrial use

XX

SQ Sequence 2991 BP; 739 A; 716 C; 695 G; 841 T; 0 U; 0 Other;

Query Match 100.0%; Score 2991; DB 4; Length 2991;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2991; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TGGTGGTGACGAGTGACGAGGATTCGCAGAAGAAAGGCCAGAACCCGATTCCTTCCCGTC 60
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Db          1 TGGTGGTGACGAGTGACGAGGATTCGCAGAAGAAAGGCCAGAACCCGATTCCTTCCCGTC 60

Qy         61 TTCTTCTCCTTCCGCCCAATTGCAGTTTTTCGCAGCGGGTCATCATCAAGACCCTCCGCC 120
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Db         61 TTCTTCTCCTTCCGCCCAATTGCAGTTTTTCGCAGCGGGTCATCATCAAGACCCTCCGCC 120

Qy        121 TTTCCGCGCCAAACGCCTTCCACCCAATCCCTCCGTTTCCCGAAATATTCCCCTTCCCTC 180
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Db        121 TTTCCGCGCCAAACGCCTTCCACCCAATCCCTCCGTTTCCCGAAATATTCCCCTTCCCTC 180

Qy        181 CCTTTTCTTCTCTACATAAACCCTAACCACCCCCATCCTCTCCTCCCGCTTCCGACCACC 240
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Db        181 CCTTTTCTTCTCTACATAAACCCTAACCACCCCCATCCTCTCCTCCCGCTTCCGACCACC 240

Qy        241 CTGCATTCTACTGGGATCCCATTTGATCGACGTTTCCCGGCGAGGATGGGCGATCACGGC 300
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Db        241 CTGCATTCTACTGGGATCCCATTTGATCGACGTTTCCCGGCGAGGATGGGCGATCACGGC 300

Qy        301 CCGAGGACCGAGATCTCGTTTGCCGGCAGTTCGCGAGCAGCATTCGCCGCTTGCTTCGCC 360
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Db        301 CCGAGGACCGAGATCTCGTTTGCCGGCAGTTCGCGAGCAGCATTCGCCGCTTGCTTCGCC 360

Qy        361 GAGCTCTGTACGATTCCGTTGGACACTGCTAAAGTTAGGCTTCAGCTCCAAAAGAAAGCA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGCTCTGTACGATTCCGTTGGACACTGCTAAAGTTAGGCTTCAGCTCCAAAAGAAAGCA 420

Qy        421 GTAACAGGTGATGTGGTGGCTTTGCCAAAATACAGGGGAATGTTGGGCACTGTTGCCACT 480
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Qy        481 ATTGCCAGGGAGGAAGGTTTGTCGGCACTCTGGAAAGGAATTGTACCCGGTTTGCATCGT 540
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Db        481 ATTGCCAGGGAGGAAGGTTTGTCGGCACTCTGGAAAGGAATTGTACCCGGTTTGCATCGT 540

Qy        541 CAATGCCTCTTTGGAGGGCTACGAATTGGGTTGTATGAACCAGTTAAGTCCTTTTATGTT 600
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Db        541 CAATGCCTCTTTGGAGGGCTACGAATTGGGTTGTATGAACCAGTTAAGTCCTTTTATGTT 600

Qy        601 GGAGATAACTTTGTTGGAGATATTCCTTTATCCAAGAAAATACTTGCTGGGCTTACAACA 660
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Db        601 GGAGATAACTTTGTTGGAGATATTCCTTTATCCAAGAAAATACTTGCTGGGCTTACAACA 660

Qy        661 GGTGCATTAGCAATTATAGTGGCAAATCCGACTGACCTTGTTAAAGTTCGACTTCAATCT 720
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Db        661 GGTGCATTAGCAATTATAGTGGCAAATCCGACTGACCTTGTTAAAGTTCGACTTCAATCT 720

Qy        721 GAAGGTAAACTCCCCCCTGGGGTACCAAGACGTTATTCAGGGGCGCTAAATGCTTATTCA 780
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Db        721 GAAGGTAAACTCCCCCCTGGGGTACCAAGACGTTATTCAGGGGCGCTAAATGCTTATTCA 780

Qy        781 ACCATAGTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCC 840
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Db        781 ACCATAGTCAAAAAGGAAGGACTTGGTGCTCTGTGGACTGGGCTTGGTCCTAATATTGCC 840

Qy        841 CGCAATGCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGATGAAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCAATGCTATTATAAATGCTGCTGAATTGGCCAGTTATGATCAAGTGAAACAGATGAAG 900

Qy        901 TCTAGAATGATGGGAGATTCAGCCTACAAAAGCACATTTGATTGTTTCATCAAGACGTTG 960
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Db        901 TCTAGAATGATGGGAGATTCAGCCTACAAAAGCACATTTGATTGTTTCATCAAGACGTTG 960

Qy        961 AAAAATGATGGGCCTCTTGCTTTTTACAAGGGGTTTATCCCAAACTTTGGTCGGTTAGGA 1020
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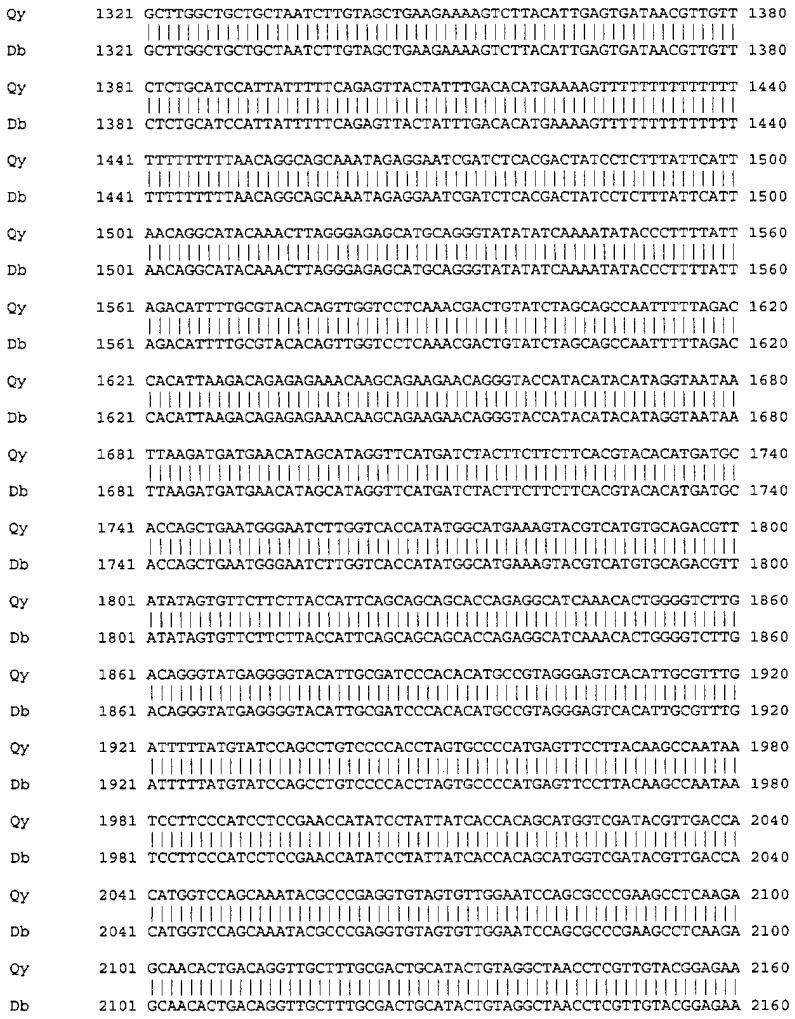
Qy       1021 TCGTGGAATGTGATCATGTTTTTGACCTTGGAGCAGGTCAAGAAGTTCTTCATCAAAGAG 1080
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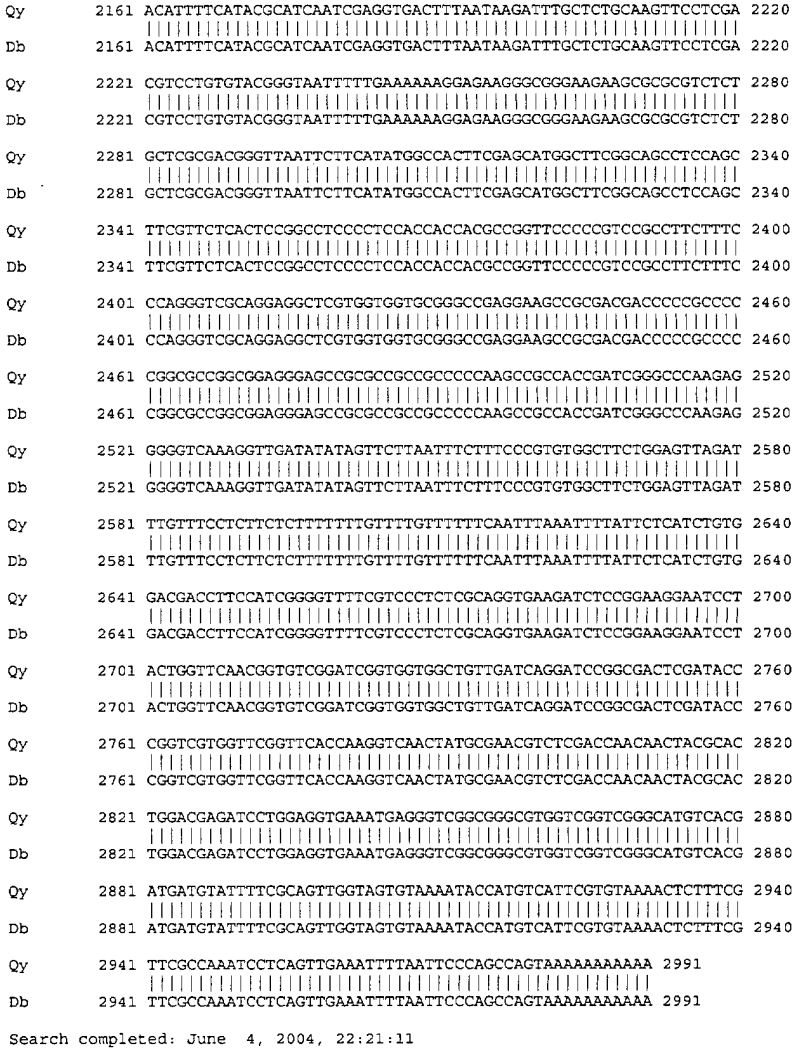
Qy       1081 GTGCCAAATTAATACATTGAAGTCGGATAGGAGTAGAAAAAAAGGGTTTTTGTGGAATTT 1140
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Db       1081 GTGCCAAATTAATACATTGAAGTCGGATAGGAGTAGAAAAAAAGGGTTTTTGTGGAATTT 1140

Qy       1141 TCTCTACCGGTGTGGATCCTGGCGAGAGAGAATAAATCTTCCTGACTGCTCAGATGTTGT 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCTCTACCGGTGTGGATCCTGGCGAGAGAGAATAAATCTTCCTGACTGCTCAGATGTTGT 1200

Qy       1201 ACCTTTTTTATGAATGGTTCTTTTCTTATAGAGGACAGAGAAAATAAAAGAAAAATTCAT 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 ACCTTTTTTATGAATGGTTCTTTTCTTATAGAGGACAGAGAAAATAAAAGAAAAATTCAT 1260

Qy       1261 TGTCATGTACTCTTTTTCCCCATTTCTGCTGAGTAGCAGCTATACCAAGCAGACTTTGTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGTCATGTACTCTTTTTCCCCATTTCTGCTGAGTAGCAGCTATACCAAGCAGACTTTGTT 1320
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Search completed: June 4, 2004, 22:21:11

Job time : 1123.97 secs

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OM nucleic - nucleic search, using sw model

Run on: June 4, 2004, 21:05:07 ; Search time 7571.55 Seconds
(without alignments)
11796.502 Million cell updates/sec

Title: US-10-671-628-3
Perfect score: 2991
Sequence: 1 tggtggtgacgagtgacgag.....ccagccagtaaaaaaaaaaa 2991

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	400.4	13.4	762	14	CF213174	CF213174 CGF100063
2	381	12.7	871	14	CB290646	CB290646 UCRCS01_0
3	365.2	12.2	1241	14	CB330501	CB330501 SpEST485
4	363.2	12.1	682	14	CF436214	CF436214 EST672559
5	363.2	12.1	719	14	CF445646	CF445646 EST681991
6	363.2	12.1	779	14	CF448435	CF448435 EST684780
7	361.2	12.1	712	14	CF452690	CF452690 EST689035
8	361	12.1	733	13	BQ972958	BQ972958 QHI11G22.
9	360	12.0	649	14	CF442797	CF442797 EST679142
10	332.6	11.1	872	12	BG446588	BG446588 GA__Eb003
11	332	11.1	747	14	CD841700	CD841700 RFO2.124F
12	330.4	11.0	679	12	BG450507	BG450507 NF019G07D
13	325.6	10.9	769	14	CD829664	CD829664 BN40.042N
14	314.2	10.5	716	14	CD820766	CD820766 BN20.053M
15	311.6	10.4	709	13	BQ842169	BQ842169 WHE2989_F
16	311.6	10.4	766	13	BQ483475	BQ483475 WHE3509_A
17	310.8	10.4	816	14	CD818539	CD818539 BN20.045M
18	310	10.4	700	14	CD894584	CD894584 G118.126J
19	310	10.4	703	14	CD934959	CD934959 OV.002H09
20	307.4	10.3	768	12	BG321351	BG321351 Ds01_07d1
21	303.4	10.1	716	10	BE454099	BE454099 HVSMEh008
22	300.8	10.1	569	12	BM093699	BM093699 saj13b05.
23	299	10.0	706	13	BQ802519	BQ802519 WHE2826_H
24	295.8	9.9	994	12	BG416382	BG416382 HVSMEk001
25	295.6	9.9	746	14	CD826833	CD826833 BN25.065D
26	293	9.8	610	13	BQ967986	BQ967986 QHB32H05.
27	292.8	9.8	742	12	BI979018	BI979018 zH02 Old
28	292	9.8	821	10	BE641808	BE641808 Cri2_4_F0
29	287.2	9.6	746	14	CF089986	CF089986 QHM3D13.y
30	285.4	9.5	736	14	CF133319	CF133319 WHE4356_E
31	280.6	9.4	481	12	BM360469	BM360469 GA__Ea003
32	279.4	9.3	897	10	BE055609	BE055609 GA__Ea003
33	276.8	9.3	676	12	BI955063	BI955063 HVSMEm002
34	276	9.2	711	12	BG366223	BG366223 HVSMEi000
35	276	9.2	793	10	BF627513	BF627513 HVSMEb000
36	275.8	9.2	757	13	BU010668	BU010668 QGJ14C11.
37	275.8	9.2	1447	13	BU103700	BU103700 SCEPAM201
38	275.4	9.2	639	14	CD825105	CD825105 BN25.059L
39	273.8	9.2	535	12	BM520694	BM520694 sak97d07.
40	273.2	9.1	1422	11	AY105357	AY105357 Zea mays
41	273	9.1	470	9	AI162254	AI162254 A014P69U
42	272.6	9.1	797	13	BQ743348	BQ743348 WHE4102_H
43	272.2	9.1	647	13	BU997263	BU997263 HI07H02r
44	270.2	9.0	642	10	BE601596	BE601596 HVSMEh009
45	269.4	9.0	650	13	CA015462	CA015462 HT14G05r

Search completed: June 5, 2004, 06:21:15
Job time : 7575.55 secs